

SEQUENCE LISTING

<110> Sprecher, Cindy A.
 Novak, Julia E.
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<120> SOLUBLE ZALPHA11 CYTOKINE RECEPTORS

<130> 00-22

<150> US 60/194,731

<151> 2000-04-05

<150> US 60/222,121

<151> 2000-07-28

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<170> FastSEQ for Windows Version 3.0

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<212> DNA

<213> Homo sapiens

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Gly	Trp	Gly	Cys	Pro	Asp	Leu	Val	Cys	Tyr	Thr	Asp	Tyr	Leu	Gln	Thr	
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gtc	atc	tgc	atc	ctg	gaa	atg	tgg	aac	ctc	cac	ccc	agc	acg	ctc	acc	144
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Cys	Ser	Leu	His	Arg	Ser	Ala	His	Asn	Ala	Thr	His	Ala	Thr	Tyr	Thr		
	65				70				75					80			
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Cys	His	Met	Asp	Val	Phe	His	Phe	Met	Ala	Asp	Asp	Ile	Phe	Ser	Val		
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Asn	Ile	Thr	Asp	Gln	Ser	Gly	Asn	Tyr	Ser	Gln	Glu	Cys	Gly	Ser	Phe		
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Leu	Leu	Ala	Glu	Ser	Ile	Lys	Pro	Ala	Pro	Pro	Phe	Asn	Val	Thr	Val		
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acc	ttc	tca	gga	cag	tat	aat	atc	tcc	tgg	cgc	tca	gat	tac	gaa	gac		432
Thr	Phe	Ser	Gly	Gln	Tyr	Asn	Ile	Ser	Trp	Arg	Ser	Asp	Tyr	Glu	Asp		
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cct	gcc	ttc	tac	atg	ctg	aag	ggc	aag	ctt	cag	tat	gag	ctg	cag	tac		480
Pro	Ala	Phe	Tyr	Met	Leu	Lys	Gly	Lys	Leu	Gln	Tyr	Glu	Leu	Gln	Tyr		
	145				150				155					160			
agg	aac	cgg	gga	gac	ccc	tgg	gct	gtg	agt	ccg	agg	aga	aag	ctg	atc		528
Arg	Asn	Arg	Gly	Asp	Pro	Trp	Ala	Val	Ser	Pro	Arg	Arg	Lys	Leu	Ile		
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Ser	Val	Asp	Ser	Arg	Ser	Val	Ser	Leu	Leu	Pro	Leu	Glu	Phe	Arg	Lys		
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gac	tcg	agc	tat	gag	ctg	cag	gtg	cgg	gca	ggg	ccc	atg	cct	ggc	tcc		624
Asp	Ser	Ser	Tyr	Glu	Leu	Gln	Val	Arg	Ala	Gly	Pro	Met	Pro	Gly	Ser		
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tcc Ser	tac Tyr	cag Gln	ggg Gly	acc Thr	tgg Trp	agt Ser	gaa Glu	tgg Trp	agt Ser	gac Asp	ccg Pro	gtc Val	atc Ile	ttt Phe	cag Gln	672
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225			230			235										
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275			280			285										
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290			295			300										
ccc Pro	tgg Trp	agc Ser	cca Pro	gag Glu	gtg Val	ccc Pro	tcc Ser	acc Thr	ctg Leu	gag Glu	gtg Val	tac Tyr	agc Ser	tgc Cys	cac His	960
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340			345			350										
ccg Pro	aca Thr	gcc Ala	cag Gln	aac Asn	tcg Ser	ggg Gly	ggc Gly	tca Ser	gct Ala	tac Tyr	agt Ser	gag Glu	gag Glu	agg Arg	gat Asp	1104
355			360			365										
cgg Arg	cca Pro	tac Tyr	ggc Gly	ctg Leu	gtg Val	tcc Ser	att Ile	gac Asp	aca Thr	gtg Val	act Thr	gtg Val	cta Leu	gat Asp	gca Ala	1152
370			375			380										

gag ggg cca tgc acc tgg ccc tgc agc tgt gag gat gac ggc tac cca	1200
Glu Gly Pro Cys Thr Trp Pro Cys Ser Cys Glu Asp Asp Gly Tyr Pro	
385 390 395 400	
gcc ctg gac ctg gat gct ggc ctg gag ccc agc cca ggc cta gag gac	1248
Ala Leu Asp Leu Asp Ala Gly Leu Glu Pro Ser Pro Gly Leu Glu Asp	
405 410 415	
cca ctc ttg gat gca ggg acc aca gtc ctg tcc tgt ggc tgt gtc tca	1296
Pro Leu Leu Asp Ala Gly Thr Thr Val Leu Ser Cys Gly Cys Val Ser	
420 425 430	
gct ggc agc cct ggg cta gga ggg ccc ctg gga agc ctc ctg gac aga	1344
Ala Gly Ser Pro Gly Leu Gly Gly Pro Leu Gly Ser Leu Leu Asp Arg	
435 440 445	
cta aag cca ccc ctt gca gat ggg gag gac tgg gct ggg gga ctg ccc	1392
Leu Lys Pro Pro Leu Ala Asp Gly Glu Asp Trp Ala Gly Gly Leu Pro	
450 455 460	
tgg ggt ggc cgg tca cct gga ggg gtc tca gag agt gag gcg ggc tca	1440
Trp Gly Gly Arg Ser Pro Gly Gly Val Ser Glu Ser Glu Ala Gly Ser	
465 470 475 480	
ccc ctg gcc ggc ctg gat atg gac acg ttt gac agt ggc ttt gtg ggc	1488
Pro Leu Ala Gly Leu Asp Met Asp Thr Phe Asp Ser Gly Phe Val Gly	
485 490 495	
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Ser Asp Cys Ser Ser Pro Val Glu Cys Asp Phe Thr Ser Pro Gly Asp	
500 505 510	
gaa gga ccc ccc cgg agc tac ctc cgc cag tgg gtg gtc att cct ccg	1584
Glu Gly Pro Pro Arg Ser Tyr Leu Arg Gln Trp Val Val Ile Pro Pro	
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<211> 538

<213> Homo sapiens

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		20						25					30		
Val	Ile	Cys	Ile	Leu	Glu	Met	Trp	Asn	Leu	His	Pro	Ser	Thr	Leu	Thr
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Leu	Thr	Trp	Gln	Asp	Gln	Tyr	Glu	Glu	Leu	Lys	Asp	Glu	Ala	Thr	Ser
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Cys	Ser	Leu	His	Arg	Ser	Ala	His	Asn	Ala	Thr	His	Ala	Thr	Tyr	Thr
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Cys	His	Met	Asp	Val	Phe	His	Phe	Met	Ala	Asp	Asp	Ile	Phe	Ser	Val
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Asn	Ile	Thr	Asp	Gln	Ser	Gly	Asn	Tyr	Ser	Gln	Glu	Cys	Gly	Ser	Phe
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Leu	Leu	Ala	Glu	Ser	Ile	Lys	Pro	Ala	Pro	Pro	Phe	Asn	Val	Thr	Val
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Thr	Phe	Ser	Gly	Gln	Tyr	Asn	Ile	Ser	Trp	Arg	Ser	Asp	Tyr	Glu	Asp
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Ser	Val	Asp	Ser	Arg	Ser	Val	Ser	Leu	Leu	Pro	Leu	Glu	Phe	Arg	Lys
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Asp	Ser	Ser	Tyr	Glu	Leu	Gln	Val	Arg	Ala	Gly	Pro	Met	Pro	Gly	Ser
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Thr	Gln	Ser	Glu	Glu	Leu	Lys	Glu	Gly	Trp	Asn	Pro	His	Leu	Leu	Leu
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Pro Trp Ser Pro Glu Val Pro Ser Thr Leu Glu Val Tyr Ser Cys His
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 Pro Pro Arg Ser Pro Ala Lys Arg Leu Gln Leu Thr Glu Leu Gln Glu
 325 330 335
 Pro Ala Glu Leu Val Glu Ser Asp Gly Val Pro Lys Pro Ser Phe Trp
 340 345 350
 Pro Thr Ala Gln Asn Ser Gly Gly Ser Ala Tyr Ser Glu Glu Arg Asp
 355 360 365
 Arg Pro Tyr Gly Leu Val Ser Ile Asp Thr Val Thr Val Leu Asp Ala
 370 375 380
 Glu Gly Pro Cys Thr Trp Pro Cys Ser Cys Glu Asp Asp Gly Tyr Pro
 385 390 395 400
 Ala Leu Asp Leu Asp Ala Gly Leu Glu Pro Ser Pro Gly Leu Glu Asp
 405 410 415
 Pro Leu Leu Asp Ala Gly Thr Thr Val Leu Ser Cys Gly Cys Val Ser
 420 425 430
 Ala Gly Ser Pro Gly Leu Gly Gly Pro Leu Gly Ser Leu Leu Asp Arg
 435 440 445
 Leu Lys Pro Pro Leu Ala Asp Gly Glu Asp Trp Ala Gly Gly Leu Pro
 450 455 460
 Trp Gly Gly Arg Ser Pro Gly Gly Val Ser Glu Ser Glu Ala Gly Ser
 465 470 475 480
 Pro Leu Ala Gly Leu Asp Met Asp Thr Phe Asp Ser Gly Phe Val Gly
 485 490 495
 Ser Asp Cys Ser Ser Pro Val Glu Cys Asp Phe Thr Ser Pro Gly Asp
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 515 520 525
 Pro Leu Ser Ser Pro Gly Pro Gln Ala Ser
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Asp	Phe	Phe	Leu	Thr	Thr	Met	Pro	Thr	Asp	Ser	Leu	Ser	Val	Ser	Thr	
			20					25					30			
ctg	ccc	ctc	cca	gag	gtt	cag	tgt	ttt	gtg	ttc	aat	gtc	gag	tac	atg	144
Leu	Pro	Leu	Pro	Glu	Val	Gln	Cys	Phe	Val	Phe	Asn	Val	Glu	Tyr	Met	
			35				40					45				
aat	tgc	act	tgg	aac	agc	agc	tct	gag	ccc	cag	cct	acc	aac	ctc	act	192
Asn	Cys	Thr	Trp	Asn	Ser	Ser	Ser	Glu	Pro	Gln	Pro	Thr	Asn	Leu	Thr	
	50					55					60					
ctg	cat	tat	tgg	tac	aag	aac	tcg	gat	aat	gat	aaa	gtc	cag	aag	tgc	240
Leu	His	Tyr	Trp	Tyr	Lys	Asn	Ser	Asp	Asn	Asp	Lys	Val	Gln	Lys	Cys	
	65				70				75						80	
agc	cac	tat	cta	ttc	tct	gaa	gaa	atc	act	tct	ggc	tgt	cag	ttg	caa	288
Ser	His	Tyr	Leu	Phe	Ser	Glu	Glu	Ile	Thr	Ser	Gly	Cys	Gln	Leu	Gln	
				85				90						95		
aaa	aag	gag	atc	cac	ctc	tac	caa	aca	ttt	gtt	gtt	cag	ctc	cag	gac	336
Lys	Lys	Glu	Ile	His	Leu	Tyr	Gln	Thr	Phe	Val	Val	Gln	Leu	Gln	Asp	
			100					105					110			
cca	cgg	gaa	ccc	agg	aga	cag	gcc	aca	cag	atg	cta	aaa	ctg	cag	aat	384
Pro	Arg	Glu	Pro	Arg	Arg	Gln	Ala	Thr	Gln	Met	Leu	Lys	Leu	Gln	Asn	
			115				120					125				
ctg	gtg	atc	ccc	tgg	gct	cca	gag	aac	cta	aca	ctt	cac	aaa	ctg	agt	432
Leu	Val	Ile	Pro	Trp	Ala	Pro	Glu	Asn	Leu	Thr	Leu	His	Lys	Leu	Ser	
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gaa	tcc	cag	cta	gaa	ctg	aac	tgg	aac	aac	aga	ttc	ttg	aac	cac	tgt	480
Glu	Ser	Gln	Leu	Glu	Leu	Asn	Trp	Asn	Asn	Arg	Phe	Leu	Asn	His	Cys	
	145				150				155						160	
ttg	gag	cac	ttg	gtg	cag	tac	cgg	act	gac	tgg	gac	cac	agc	tgg	act	528
Leu	Glu	His	Leu	Val	Gln	Tyr	Arg	Thr	Asp	Trp	Asp	His	Ser	Trp	Thr	
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 180 185 190

ggg cag aaa cgc tac acg ttt cgt gtt cgg agc cgc ttt aac cca ctc 624
 Gly Gln Lys Arg Tyr Thr Phe Arg Val Arg Ser Arg Phe Asn Pro Leu
 195 200 205

tgt gga agt gct cag cat tgg agt gaa tgg agc cac cca atc cac tgg 672
 Cys Gly Ser Ala Gln His Trp Ser Glu Trp Ser His Pro Ile His Trp
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<212> PRT

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 35 40 45
 Asn Cys Thr Trp Asn Ser Ser Ser Glu Pro Gln Pro Thr Asn Leu Thr
 50 55 60
 Leu His Tyr Trp Tyr Lys Asn Ser Asp Asn Asp Lys Val Gln Lys Cys
 65 70 75 80
 Ser His Tyr Leu Phe Ser Glu Glu Ile Thr Ser Gly Cys Gln Leu Gln
 85 90 95
 Lys Lys Glu Ile His Leu Tyr Gln Thr Phe Val Val Gln Leu Gln Asp
 100 105 110
 Pro Arg Glu Pro Arg Arg Gln Ala Thr Gln Met Leu Lys Leu Gln Asn
 115 120 125
 Leu Val Ile Pro Trp Ala Pro Glu Asn Leu Thr Leu His Lys Leu Ser
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1				5					10					15		
atc	ctg	gaa	atg	tgg	aac	ctc	cac	ccc	agc	acg	ctc	acc	ctt	acc	tgg	96
Ile	Leu	Glu	Met	Trp	Asn	Leu	His	Pro	Ser	Thr	Leu	Thr	Leu	Thr	Trp	
			20					25					30			
caa	gac	cag	tat	gaa	gag	ctg	aag	gac	gag	gcc	acc	tcc	tgc	agc	ctc	144
Gln	Asp	Gln	Tyr	Glu	Glu	Leu	Lys	Asp	Glu	Ala	Thr	Ser	Cys	Ser	Leu	
		35					40					45				
cac	agg	tcg	gcc	cac	aat	gcc	acg	cat	gcc	acc	tac	acc	tgc	cac	atg	192
His	Arg	Ser	Ala	His	Asn	Ala	Thr	His	Ala	Thr	Tyr	Thr	Cys	His	Met	
	50					55					60					
gat	gta	ttc	cac	ttc	atg	gcc	gac	gac	att	ttc	agt	gtc	aac	atc	aca	240
Asp	Val	Phe	His	Phe	Met	Ala	Asp	Asp	Ile	Phe	Ser	Val	Asn	Ile	Thr	
65					70					75					80	
gac	cag	tct	ggc	aac	tac	tcc	cag	gag	tgt	ggc	agc	ttt	ctc	ctg	gct	288

Cys Pro Asp Leu Val Cys Tyr Thr Asp Tyr Leu Gln Thr Val Ile Cys
1 5 10 15

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Ile Leu Glu Met Trp Asn Leu His Pro Ser Thr Leu Thr Leu Thr Trp
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His Arg Ser Ala His Asn Ala Thr His Ala Thr Tyr Thr Cys His Met
      50                55                60
Asp Val Phe His Phe Met Ala Asp Asp Ile Phe Ser Val Asn Ile Thr
      65                70                75                80
Asp Gln Ser Gly Asn Tyr Ser Gln Glu Cys Gly Ser Phe Leu Leu Ala
      85                90                95
Glu Ser Ile Lys Pro Ala Pro Pro Phe Asn Val Thr Val Thr Phe Ser
      100               105               110
Gly Gln Tyr Asn Ile Ser Trp Arg Ser Asp Tyr Glu Asp Pro Ala Phe
      115               120               125
Tyr Met Leu Lys Gly Lys Leu Gln Tyr Glu Leu Gln Tyr Arg Asn Arg
      130               135               140
Gly Asp Pro Trp Ala Val Ser Pro Arg Arg Lys Leu Ile Ser Val Asp
      145               150               155               160
Ser Arg Ser Val Ser Leu Leu Pro Leu Glu Phe Arg Lys Asp Ser Ser
      165               170               175
Tyr Glu Leu Gln Val Arg Ala Gly Pro Met Pro Gly Ser Ser Tyr Gln
      180               185               190
Gly Thr Trp Ser Glu Trp Ser Asp Pro Val Ile Phe Gln Thr Gln Ser
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Glu Glu Leu Lys Glu Gly Trp Asn Pro His
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<212> DNA

<213> Artificial Sequence

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<223> Degenerate polynucleotide sequence of soluble
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 NO:6

<221> misc_feature

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<223> n = A,T,C or G

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gaygargcna	cnwsntgyws	nytncaymgn	wsngcncaya	aygcnacnca	ygcnacntay	180
acntgycaya	tggaygtntt	ycayttyatg	gcngaygaya	thttywsngt	naayathacn	240
gaycarwsng	gnaaytayws	ncargartgy	ggngwsntty	tnytngcnga	rwsnathaar	300
ccngcncnc	cnttyaaygt	nacngtnacn	ttywsnggnc	artayaayat	hwsntggmgn	360
wsngaytayg	argayccngc	nttytayatg	ytnaarggna	arytncarta	ygarytnear	420
taymgnaaym	gnggngaycc	ntgggcngtn	wsnccnmgnm	gnaarytnat	hwsngtngay	480
wsnmgngwsng	tnwsnytnyt	nccnytngar	ttymgnaarg	aywsnwsnta	ygarytnear	540
gtmgngcng	gncnatgcc	nggnwsnwsn	taycarggna	cntggwsnga	rtggwsngay	600
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tttgtnttya	aygtngarta	yatgaaytgy	acntggaayw	snwsnwsnga	rcncarccn	180
acnaayytna	cnytncayta	ytggtayaar	aaywsngaya	aygayaargt	ncaraartgy	240
wsncaytayy	tnttywsnga	rgarathacn	wsnggntgy	arytncaraa	raargarath	300
cayytntayc	aracnttygt	ngtncarytn	cargayccnm	gngarccnm	nmgncargcn	360
acncaratgy	tnaarytnca	raayytngtn	athccntggg	cncngaraa	yytnacnytn	420
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<212> DNA
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Val Ile Phe Leu Gly Thr Leu Val His Lys Ser Ser Ser Gln Gly Gln	
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Asp Arg His Met Ile Arg Met Arg Gln Leu Ile Asp Ile Val Asp Gln	
35 40 45	
ctg aaa aat tat gtg aat gac ttg gtc cct gaa ttt ctg cca gct cca	192
Leu Lys Asn Tyr Val Asn Asp Leu Val Pro Glu Phe Leu Pro Ala Pro	
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Glu Asp Val Glu Thr Asn Cys Glu Trp Ser Ala Phe Ser Cys Phe Gln	
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Lys Ala Gln Leu Lys Ser Ala Asn Thr Gly Asn Asn Glu Arg Ile Ile	
85 90 95	
aat gta tca att aaa aag ctg aag agg aaa cca cct tcc aca aat gca	336
Asn Val Ser Ile Lys Lys Leu Lys Arg Lys Pro Pro Ser Thr Asn Ala	
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ggg aga aga cag aaa cac aga cta aca tgc cct tca tgt gat tct tat	384
Gly Arg Arg Gln Lys His Arg Leu Thr Cys Pro Ser Cys Asp Ser Tyr	
115 120 125	
gag aaa aaa cca ccc aaa gaa ttc cta gaa aga ttc aaa tca ctt ctc	432
Glu Lys Lys Pro Pro Lys Glu Phe Leu Glu Arg Phe Lys Ser Leu Leu	
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 Asp Ser

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 Leu Lys Asn Tyr Val Asn Asp Leu Val Pro Glu Phe Leu Pro Ala Pro
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 Glu Asp Val Glu Thr Asn Cys Glu Trp Ser Ala Phe Ser Cys Phe Gln
 65 70 75 80
 Lys Ala Gln Leu Lys Ser Ala Asn Thr Gly Asn Asn Glu Arg Ile Ile
 85 90 95
 Asn Val Ser Ile Lys Lys Leu Lys Arg Lys Pro Pro Ser Thr Asn Ala
 100 105 110
 Gly Arg Arg Gln Lys His Arg Leu Thr Cys Pro Ser Cys Asp Ser Tyr
 115 120 125
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Met Pro Arg Gly Pro Val Ala Ala Leu Leu	
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Leu Leu Ile Leu His Gly Ala Trp Ser Cys Leu Asp Leu Thr Cys Tyr	
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act gac tac ctc tgg acc atc acc tgt gtc ctg gag aca cgg agc ccc	268
Thr Asp Tyr Leu Trp Thr Ile Thr Cys Val Leu Glu Thr Arg Ser Pro	
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Asn Pro Ser Ile Leu Ser Leu Thr Trp Gln Asp Glu Tyr Glu Glu Leu	
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cag gac caa gag acc ttc tgc agc cta cac agg tct ggc cac aac acc	364
Gln Asp Gln Glu Thr Phe Cys Ser Leu His Arg Ser Gly His Asn Thr	
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aca cat ata tgg tac acg tgc cat atg cgc ttg tct caa ttc ctg tcc	412
Thr His Ile Trp Tyr Thr Cys His Met Arg Leu Ser Gln Phe Leu Ser	
75 80 85 90	
gat gaa gtt ttc att gtc aat gtg acg gac cag tct ggc aac aac tcc	460
Asp Glu Val Phe Ile Val Asn Val Thr Asp Gln Ser Gly Asn Asn Ser	
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caa gag tgt ggc agc ttt gtc ctg gct gag agc atc aaa cca gct ccc	508
Gln Glu Cys Gly Ser Phe Val Leu Ala Glu Ser Ile Lys Pro Ala Pro	
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ccc ttg aac gtg act gtg gcc ttc tca gga cgc tat gat atc tcc tgg	556
Pro Leu Asn Val Thr Val Ala Phe Ser Gly Arg Tyr Asp Ile Ser Trp	
125 130 135	
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Gln	Tyr	Glu	Leu	Gln	Tyr	Arg	Asn	Leu	Arg	Asp	Pro	Tyr	Ala	Val	Arg	
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Pro	Glu	Glu	Phe	His	Lys	Asp	Ser	Ser	Tyr	Gln	Leu	Gln	Val	Arg	Ala	
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Asp	Pro	Val	Ile	Phe	Gln	Thr	Gln	Ala	Gly	Glu	Pro	Glu	Ala	Gly	Trp	
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gac	cct	cac	atg	ctg	ctg	ctc	ctg	gct	gtc	ttg	atc	att	gtc	ctg	gtt	892
Asp	Pro	His	Met	Leu	Leu	Leu	Leu	Ala	Val	Leu	Ile	Ile	Val	Leu	Val	
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ttc	atg	ggt	ctg	aag	atc	cac	ctg	cct	tgg	agg	cta	tgg	aaa	aag	ata	940
Phe	Met	Gly	Leu	Lys	Ile	His	Leu	Pro	Trp	Arg	Leu	Trp	Lys	Lys	Ile	
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Trp	Ala	Pro	Val	Pro	Thr	Pro	Glu	Ser	Phe	Phe	Gln	Pro	Leu	Tyr	Arg	
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Glu	His	Ser	Gly	Asn	Phe	Lys	Lys	Trp	Val	Asn	Thr	Pro	Phe	Thr	Ala	
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Ser	Ser	Ile	Glu	Leu	Val	Pro	Gln	Ser	Ser	Thr	Thr	Thr	Ser	Ala	Leu	
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Gly	Leu	Glu	Glu	Gln	Leu	Glu	Cys	Asp	Gly	Met	Ser	Glu	Pro	Gly	His	
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Trp	Cys	Ile	Ile	Pro	Leu	Ala	Ala	Gly	Gln	Ala	Val	Ser	Ala	Tyr	Ser	
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gag	gag	aga	gac	cgg	cca	tat	ggt	ctg	gtg	tcc	att	gac	aca	gtg	act	1276
Glu	Glu	Arg	Asp	Arg	Pro	Tyr	Gly	Leu	Val	Ser	Ile	Asp	Thr	Val	Thr	
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gtg	gga	gat	gca	gag	ggc	ctg	tgt	gtc	tgg	ccc	tgt	agc	tgt	gag	gat	1324
Val	Gly	Asp	Ala	Glu	Gly	Leu	Cys	Val	Trp	Pro	Cys	Ser	Cys	Glu	Asp	
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gat	ggc	tat	cca	gcc	atg	aac	ctg	gat	gct	ggc	cga	gag	tct	ggc	cct	1372
Asp	Gly	Tyr	Pro	Ala	Met	Asn	Leu	Asp	Ala	Gly	Arg	Glu	Ser	Gly	Pro	
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aat	tca	gag	gat	ctg	ctc	ttg	gtc	aca	gac	cct	gct	ttt	ctg	tct	tgc	1420
Asn	Ser	Glu	Asp	Leu	Leu	Leu	Val	Thr	Asp	Pro	Ala	Phe	Leu	Ser	Cys	
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Gly	Cys	Val	Ser	Gly	Ser	Gly	Leu	Arg	Leu	Gly	Gly	Ser	Pro	Gly	Ser	
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Leu	Leu	Asp	Arg	Leu	Arg	Leu	Ser	Phe	Ala	Lys	Glu	Gly	Asp	Trp	Thr	
		445					450					455				
gca	gac	cca	acc	tgg	aga	act	ggg	tcc	cca	gga	ggg	ggc	tct	gag	agt	1564
Ala	Asp	Pro	Thr	Trp	Arg	Thr	Gly	Ser	Pro	Gly	Gly	Gly	Ser	Glu	Ser	
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Val	Leu	Ala	Glu	Ser	Ile	Lys	Pro	Ala	Pro	Pro	Leu	Asn	Val	Thr	Val																
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Arg	Asn	Leu	Arg	Asp 165	Pro	Tyr	Ala	Val	Arg	Pro	Val	Thr	Lys	Leu	Ile
Ser	Val	Asp	Ser	Arg	Asn	Val	Ser	Leu	Leu	Pro	Glu	Glu	Phe	His	Lys
Asp	Ser	Ser	Tyr	Gln	Leu	Gln	Val	Arg	Ala	Ala	Pro	Gln	Pro	Gly	Thr
Ser	Phe	Arg	Gly	Thr	Trp	Ser	Glu	Trp	Ser	Asp	Pro	Val	Ile	Phe	Gln
Thr	Gln	Ala	Gly	Glu	Pro	Glu	Ala	Gly	Trp	Asp	Pro	His	Met	Leu	Leu
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Leu	Leu	Ala	Val	Leu	Ile	Ile	Val	Leu	Val	Phe	Met	Gly	Leu	Lys	Ile
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His	Leu	Pro	Trp	Arg	Leu	Trp	Lys	Lys	Ile	Trp	Ala	Pro	Val	Pro	Thr
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Pro	Glu	Ser	Phe	Phe	Gln	Pro	Leu	Tyr	Arg	Glu	His	Ser	Gly	Asn	Phe
Lys	Lys	Trp	Val	Asn	Thr	Pro	Phe	Thr	Ala	Ser	Ser	Ile	Glu	Leu	Val
Pro	Gln	Ser	Ser	Thr	Thr	Thr	Ser	Ala	Leu	His	Leu	Ser	Leu	Tyr	Pro
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Ala	Lys	Glu	Lys	Lys	Phe	Pro	Gly	Leu	Pro	Gly	Leu	Glu	Glu	Gln	Leu
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Glu	Cys	Asp	Gly	Met	Ser	Glu	Pro	Gly	His	Trp	Cys	Ile	Ile	Pro	Leu
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Ala	Ala	Gly	Gln	Ala	Val	Ser	Ala	Tyr	Ser	Glu	Glu	Arg	Asp	Arg	Pro
Tyr	Gly	Leu	Val	Ser	Ile	Asp	Thr	Val	Thr	Val	Gly	Asp	Ala	Glu	Gly
Leu	Cys	Val	Trp	Pro	Cys	Ser	Cys	Glu	Asp	Asp	Gly	Tyr	Pro	Ala	Met
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Asn	Leu	Asp	Ala	Gly	Arg	Glu	Ser	Gly	Pro	Asn	Ser	Glu	Asp	Leu	Leu
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Leu	Val	Thr	Asp	Pro	Ala	Phe	Leu	Ser	Cys	Gly	Cys	Val	Ser	Gly	Ser
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Gly	Leu	Asp	Met	Asp	Thr	Phe	Asp	Ser	Gly	Phe	Ala	Gly	Ser	Asp	Cys
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<210> 14
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 <212> PRT
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<220>
 <223> Glu-Glu (CEE) Tag amino acid sequence

<400> 14
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Gly Trp Gly Cys Pro Asp Leu Val Cys Tyr Thr Asp Tyr Leu Gln Thr	
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gtc atc tgc atc ctg gaa atg tgg aac ctc cac ccc agc acg ctc acc	144
Val Ile Cys Ile Leu Glu Met Trp Asn Leu His Pro Ser Thr Leu Thr	
35 40 45	
ctt acc tgg caa gac cag tat gaa gag ctg aag gac gag gcc acc tcc	192
Leu Thr Trp Gln Asp Gln Tyr Glu Glu Leu Lys Asp Glu Ala Thr Ser	
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Cys Ser Leu His Arg Ser Ala His Asn Ala Thr His Ala Thr Tyr Thr	
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Cys His Met Asp Val Phe His Phe Met Ala Asp Asp Ile Phe Ser Val	
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aac atc aca gac cag tct ggc aac tac tcc cag gag tgt ggc agc ttt	336
Asn Ile Thr Asp Gln Ser Gly Asn Tyr Ser Gln Glu Cys Gly Ser Phe	
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ctc ctg gct gag agc atc aag ccg gct ccc cct ttc aac gtg act gtg	384
Leu Leu Ala Glu Ser Ile Lys Pro Ala Pro Pro Phe Asn Val Thr Val	
115 120 125	
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Thr Phe Ser Gly Gln Tyr Asn Ile Ser Trp Arg Ser Asp Tyr Glu Asp	
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cct gcc ttc tac atg ctg aag ggc aag ctt cag tat gag ctg cag tac	480
Pro Ala Phe Tyr Met Leu Lys Gly Lys Leu Gln Tyr Glu Leu Gln Tyr	
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Arg Asn Arg Gly Asp Pro Trp Ala Val Ser Pro Arg Arg Lys Leu Ile	
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Ser Val Asp Ser Arg Ser Val Ser Leu Leu Pro Leu Glu Phe Arg Lys	
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Asp Ser Ser Tyr Glu Leu Gln Val Arg Ala Gly Pro Met Pro Gly Ser	
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Ser Tyr Gln Gly Thr Trp Ser Glu Trp Ser Asp Pro Val Ile Phe Gln	
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Thr Gln Ser Glu Glu Leu Lys Glu Gly Trp Asn Pro His Ala Ser Thr	
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Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser	
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Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu	
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Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His	
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Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser	
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Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys	
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Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys	
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Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val	
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Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp	
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Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr	
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aac agc acg tac cgt gtg gtc agc gtc ctc acc gtc ctg cac cag gac	1296
Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp	
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Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu	
435 440 445	
cca gcc ccc atc gag aaa acc atc tcc aaa gcc aaa ggg cag ccc cga	1392
Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg	
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Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys	
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aac cag gtc agc ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac	1488
Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp	
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 Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
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acc acg cct ccc gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc 1584
 Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
 515 520 525

aag ctc acc gtg gac aag agc agg tgg cag cag ggg aac gtc ttc tca 1632
 Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser
 530 535 540

tgc tcc gtg atg cat gag gct ctg cac aac cac tac acg cag aag agc 1680
 Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
 545 550 555 560

ctc tcc ctg tct ccg ggt aaa 1701
 Leu Ser Leu Ser Pro Gly Lys
 565

<210> 16

<211> 567

<212> PRT

<213> Artificial Sequence

<400> 16

Met	Pro	Arg	Gly	Trp	Ala	Ala	Pro	Leu	Leu	Leu	Leu	Leu	Gln	Gly	
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Gly	Trp	Gly	Cys	Pro	Asp	Leu	Val	Cys	Tyr	Thr	Asp	Tyr	Leu	Gln	Thr
			20					25					30		
Val	Ile	Cys	Ile	Leu	Glu	Met	Trp	Asn	Leu	His	Pro	Ser	Thr	Leu	Thr
			35				40					45			
Leu	Thr	Trp	Gln	Asp	Gln	Tyr	Glu	Glu	Leu	Lys	Asp	Glu	Ala	Thr	Ser
			50			55					60				
Cys	Ser	Leu	His	Arg	Ser	Ala	His	Asn	Ala	Thr	His	Ala	Thr	Tyr	Thr
65					70				75					80	
Cys	His	Met	Asp	Val	Phe	His	Phe	Met	Ala	Asp	Asp	Ile	Phe	Ser	Val
				85					90					95	
Asn	Ile	Thr	Asp	Gln	Ser	Gly	Asn	Tyr	Ser	Gln	Glu	Cys	Gly	Ser	Phe
			100				105						110		
Leu	Leu	Ala	Glu	Ser	Ile	Lys	Pro	Ala	Pro	Pro	Phe	Asn	Val	Thr	Val
			115				120						125		

Thr Phe Ser Gly Gln Tyr Asn Ile Ser Trp Arg Ser Asp Tyr Glu Asp
 130 135 140
 Pro Ala Phe Tyr Met Leu Lys Gly Lys Leu Gln Tyr Glu Leu Gln Tyr
 145 150 155 160
 Arg Asn Arg Gly Asp Pro Trp Ala Val Ser Pro Arg Arg Lys Leu Ile
 165 170 175
 Ser Val Asp Ser Arg Ser Val Ser Leu Leu Pro Leu Glu Phe Arg Lys
 180 185 190
 Asp Ser Ser Tyr Glu Leu Gln Val Arg Ala Gly Pro Met Pro Gly Ser
 195 200 205
 Ser Tyr Gln Gly Thr Trp Ser Glu Trp Ser Asp Pro Val Ile Phe Gln
 210 215 220
 Thr Gln Ser Glu Glu Leu Lys Glu Gly Trp Asn Pro His Ala Ser Thr
 225 230 235 240
 Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser
 245 250 255
 Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu
 260 265 270
 Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His
 275 280 285
 Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser
 290 295 300
 Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys
 305 310 315 320
 Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu
 325 330 335
 Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro
 340 345 350
 Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
 355 360 365
 Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
 370 375 380
 Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp
 385 390 395 400
 Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr
 405 410 415
 Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
 420 425 430
 Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu
 435 440 445
 Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
 450 455 460

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys
 465 470 475 480
 Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
 485 490 495
 Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
 500 505 510
 Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
 515 520 525
 Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser
 530 535 540
 Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
 545 550 555 560
 Leu Ser Leu Ser Pro Gly Lys
 565

<210> 17

<211> 1083

<212> DNA

<213> Artificial Sequence

<220>

<223> soluble human IL-2Rgamma/human kappa light chain
construct

<221> CDS

<222> (1)...(1083)

<400> 17

atg	ttg	aag	cca	tca	tta	cca	ttc	aca	tcc	ctc	tta	ttc	ctg	cag	ctg	48
Met	Leu	Lys	Pro	Ser	Leu	Pro	Phe	Thr	Ser	Leu	Leu	Phe	Leu	Gln	Leu	
1				5					10					15		

ccc	ctg	ctg	gga	gtg	ggg	ctg	aac	acg	aca	att	ctg	acg	ccc	aat	ggg	96
Pro	Leu	Leu	Gly	Val	Gly	Leu	Asn	Thr	Thr	Ile	Leu	Thr	Pro	Asn	Gly	
			20					25					30			

aat	gaa	gac	acc	aca	gct	gat	ttc	ttc	ctg	acc	act	atg	ccc	act	gac	144
Asn	Glu	Asp	Thr	Thr	Ala	Asp	Phe	Phe	Leu	Thr	Thr	Met	Pro	Thr	Asp	
			35				40					45				

tcc	ctc	agt	gtt	tcc	act	ctg	ccc	ctc	cca	gag	gtt	cag	tgt	ttt	gtg	192
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

Ser	Leu	Ser	Val	Ser	Thr	Leu	Pro	Leu	Pro	Glu	Val	Gln	Cys	Phe	Val		
50						55					60						
ttc	aat	gtc	gag	tac	atg	aat	tgc	act	tgg	aac	agc	agc	tct	gag	ccc	240	
Phe	Asn	Val	Glu	Tyr	Met	Asn	Cys	Thr	Trp	Asn	Ser	Ser	Ser	Glu	Pro		
65					70				75					80			
cag	cct	acc	aac	ctc	act	ctg	cat	tat	tgg	tac	aag	aac	tcg	gat	aat	288	
Gln	Pro	Thr	Asn	Leu	Thr	Leu	His	Tyr	Trp	Tyr	Lys	Asn	Ser	Asp	Asn		
				85				90					95				
gat	aaa	gtc	cag	aag	tgc	agc	cac	tat	cta	ttc	tct	gaa	gaa	atc	act	336	
Asp	Lys	Val	Gln	Lys	Cys	Ser	His	Tyr	Leu	Phe	Ser	Glu	Glu	Ile	Thr		
			100					105					110				
tct	ggc	tgt	cag	ttg	caa	aaa	aag	gag	atc	cac	ctc	tac	caa	aca	ttt	384	
Ser	Gly	Cys	Gln	Leu	Gln	Lys	Lys	Glu	Ile	His	Leu	Tyr	Gln	Thr	Phe		
			115				120					125					
gtt	gtt	cag	ctc	cag	gac	cca	cgg	gaa	ccc	agg	aga	cag	gcc	aca	cag	432	
Val	Val	Gln	Leu	Gln	Asp	Pro	Arg	Glu	Pro	Arg	Arg	Gln	Ala	Thr	Gln		
			130				135					140					
atg	cta	aaa	ctg	cag	aat	ctg	gtg	atc	ccc	tgg	gct	cca	gag	aac	cta	480	
Met	Leu	Lys	Leu	Gln	Asn	Leu	Val	Ile	Pro	Trp	Ala	Pro	Glu	Asn	Leu		
145					150					155					160		
aca	ctt	cac	aaa	ctg	agt	gaa	tcc	cag	cta	gaa	ctg	aac	tgg	aac	aac	528	
Thr	Leu	His	Lys	Leu	Ser	Glu	Ser	Gln	Leu	Glu	Leu	Asn	Trp	Asn	Asn		
				165					170					175			
aga	ttc	ttg	aac	cac	tgt	ttg	gag	cac	ttg	gtg	cag	tac	cgg	act	gac	576	
Arg	Phe	Leu	Asn	His	Cys	Leu	Glu	His	Leu	Val	Gln	Tyr	Arg	Thr	Asp		
			180					185					190				
tgg	gac	cac	agc	tgg	act	gaa	caa	tca	gtg	gat	tat	aga	cat	aag	ttc	624	
Trp	Asp	His	Ser	Trp	Thr	Glu	Gln	Ser	Val	Asp	Tyr	Arg	His	Lys	Phe		
			195				200					205					
tcc	ttg	cct	agt	gtg	gat	ggg	cag	aaa	cgc	tac	acg	ttt	cgt	gtt	cgg	672	
Ser	Leu	Pro	Ser	Val	Asp	Gly	Gln	Lys	Arg	Tyr	Thr	Phe	Arg	Val	Arg		
			210				215					220					

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agc cgc ttt aac cca ctc tgt gga agt gct cag cat tgg agt gaa tgg      720
Ser Arg Phe Asn Pro Leu Cys Gly Ser Ala Gln His Trp Ser Glu Trp
225                230                235                240

agc cac cca atc cac tgg ggg agc aat act tca aaa gag aat act gtg      768
Ser His Pro Ile His Trp Gly Ser Asn Thr Ser Lys Glu Asn Thr Val
                245                250                255

gct gca cca tct gtc ttc atc ttc ccg cca tct gat gag cag ttg aaa      816
Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys
                260                265                270

tct ggt acc gcc tct gtt gtg tgc ctg ctg aat aac ttc tat ccc aga      864
Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg
                275                280                285

gag gcc aaa gta cag tgg aag gtg gat aac gcc ctc caa tcg ggt aac      912
Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn
290                295                300

tcc cag gag agt gtc aca gag cag gac agc aag gac agc acc tac agc      960
Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser
305                310                315                320

ctc agc agc acc ctg acg ctg agc aaa gca gac tac gag aaa cac aaa      1008
Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys
                325                330                335

gtc tac gcc tgc gaa gtc acc cat cag ggc ctg agc tcg ccc gtc aca      1056
Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr
                340                345                350

aag agc ttc aac agg gga gag tgt tag      1083
Lys Ser Phe Asn Arg Gly Glu Cys *
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<210> 18

<211> 360

<212> PRT

<213> Artificial Sequence

<400> 18

Met	Leu	Lys	Pro	Ser	Leu	Pro	Phe	Thr	Ser	Leu	Leu	Phe	Leu	Gln	Leu
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Pro	Leu	Leu	Gly	Val	Gly	Leu	Asn	Thr	Thr	Ile	Leu	Thr	Pro	Asn	Gly
			20					25					30		
Asn	Glu	Asp	Thr	Thr	Ala	Asp	Phe	Phe	Leu	Thr	Thr	Met	Pro	Thr	Asp
		35					40					45			
Ser	Leu	Ser	Val	Ser	Thr	Leu	Pro	Leu	Pro	Glu	Val	Gln	Cys	Phe	Val
	50					55					60				
Phe	Asn	Val	Glu	Tyr	Met	Asn	Cys	Thr	Trp	Asn	Ser	Ser	Ser	Glu	Pro
65					70					75					80
Gln	Pro	Thr	Asn	Leu	Thr	Leu	His	Tyr	Trp	Tyr	Lys	Asn	Ser	Asp	Asn
			85						90					95	
Asp	Lys	Val	Gln	Lys	Cys	Ser	His	Tyr	Leu	Phe	Ser	Glu	Glu	Ile	Thr
		100						105						110	
Ser	Gly	Cys	Gln	Leu	Gln	Lys	Lys	Glu	Ile	His	Leu	Tyr	Gln	Thr	Phe
		115				120						125			
Val	Val	Gln	Leu	Gln	Asp	Pro	Arg	Glu	Pro	Arg	Arg	Gln	Ala	Thr	Gln
	130					135					140				
Met	Leu	Lys	Leu	Gln	Asn	Leu	Val	Ile	Pro	Trp	Ala	Pro	Glu	Asn	Leu
145					150					155					160
Thr	Leu	His	Lys	Leu	Ser	Glu	Ser	Gln	Leu	Glu	Leu	Asn	Trp	Asn	Asn
			165						170					175	
Arg	Phe	Leu	Asn	His	Cys	Leu	Glu	His	Leu	Val	Gln	Tyr	Arg	Thr	Asp
		180						185					190		
Trp	Asp	His	Ser	Trp	Thr	Glu	Gln	Ser	Val	Asp	Tyr	Arg	His	Lys	Phe
	195						200					205			
Ser	Leu	Pro	Ser	Val	Asp	Gly	Gln	Lys	Arg	Tyr	Thr	Phe	Arg	Val	Arg
	210					215					220				
Ser	Arg	Phe	Asn	Pro	Leu	Cys	Gly	Ser	Ala	Gln	His	Trp	Ser	Glu	Trp
225				230						235					240
Ser	His	Pro	Ile	His	Trp	Gly	Ser	Asn	Thr	Ser	Lys	Glu	Asn	Thr	Val
			245						250					255	
Ala	Ala	Pro	Ser	Val	Phe	Ile	Phe	Pro	Pro	Ser	Asp	Glu	Gln	Leu	Lys
		260					265						270		
Ser	Gly	Thr	Ala	Ser	Val	Val	Cys	Leu	Leu	Asn	Asn	Phe	Tyr	Pro	Arg
	275						280					285			
Glu	Ala	Lys	Val	Gln	Trp	Lys	Val	Asp	Asn	Ala	Leu	Gln	Ser	Gly	Asn
	290				295						300				
Ser	Gln	Glu	Ser	Val	Thr	Glu	Gln	Asp	Ser	Lys	Asp	Ser	Thr	Tyr	Ser
305					310					315					320

<210>	19	
<211>	36	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	Oligonucleotide primer ZC19905	
<400>	19	
acaggatccg	tcagcatgcc	gcgtggctgg gccgcc
		36
<210>	20	
<211>	33	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	Oligonucleotide primer ZC19906	
<400>	20	
acagaattct	tagctggcct	ggggtccagg cgt
		33
<210>	21	
<211>	36	
<212>	DNA	
<213>	Artificial Sequence	
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<223>	Oligonucleotide primer ZC19931	
<400>	21	
ggttggtacc	gcaagatgcc	gcgtggctgg gccgcc
		36
<210>	22	
<211>	29	

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer ZC19932

<400> 22

cggaggatcc gtgaggggttc cagccttcc

29

<210> 23

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> FLAG tag amino acid sequence

<400> 23

Asp Tyr Lys Asp Asp Asp Asp Lys
1 5

<210> 24

<211> 66

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer spanning vector flanking
region and the 5' end of the zalpha11

<400> 24

tccactttgc ctttctctcc acaggtgtcc agggaattca tcgataatgc cgcgtggctg
ggccgc

60

66

<210> 25

<211> 699

<212> DNA

<213> Homo sapiens

<400> 25

gagcccagat cttcagacaa aactcacaca tgcccaccgt gcccagcacc tgaagccgag
ggggcaccgt cagtcttcct cttcccccca aaacccaagg acaccctcat gatctcccgg
accctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc

60

120

180

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aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag 240
tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat 300
ggcaaggagt acaagtgcaa ggtctccaac aaagccctcc catcctccat cgagaaaacc 360
atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg 420
gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatcccagc 480
gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct 540
cccgtgctgg actccgacgg ctcttcttc ctctacagca agctcaccgt ggacaagagc 600
aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac 660
tacacgcaga agagcctctc cctgtctccg ggtaaataa 699

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<210> 26

<211> 62

<212> DNA

<213> Artificial Sequence

<220>

<223> First Oligonucleotide primer spanning 3' end of
the zalphall extracellular domain and the 5' end
of Fc4

<400> 26

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gcacggtggg catgtgtgag ttttgtctga agatctgggc tcgtgagggt tccagccttc 60
ct 62

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<210> 27

<211> 61

<212> DNA

<213> Artificial Sequence

<220>

<223> Second Oligonucleotide primer spanning 3' end of
the zalphall extracellular domain and the 5' end
of Fc4

<400> 27

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agacccagtc agaggagtta aaggaaggct ggaaccctca cgagcccaga tcttcagaca 60
a 61

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<210> 28

<211> 67

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer spanning the 3' end of Fc4
and the vector flanking region

<400> 28

gtgggcctct	ggggtgggta	caaccccaga	gctgttttaa	tctagattat	ttacccggag	60
acaggga						67

<210> 29

<211> 1821

<212> DNA

<213> Artificial Sequence

<220>

<223> Polynucleotide encoding MBP-human zalphall soluble
receptor fusion

<221> CDS

<222> (1)...(1821)

<400> 29

atg	aaa	atc	gaa	ggt	aaa	ctg	gta	atc	tgg	att	aac	ggc	gat	aaa	48
Met	Lys	Ile	Glu	Glu	Gly	Lys	Leu	Val	Ile	Trp	Ile	Asn	Gly	Asp	Lys
1			5					10					15		

ggc	tat	aac	ggt	ctc	gct	gaa	gtc	ggt	aag	aaa	ttc	gag	aaa	gat	acc	96
Gly	Tyr	Asn	Gly	Leu	Ala	Glu	Val	Gly	Lys	Lys	Phe	Glu	Lys	Asp	Thr	
			20					25					30			

gga	att	aaa	gtc	acc	gtt	gag	cat	ccg	gat	aaa	ctg	gaa	gag	aaa	ttc	144
Gly	Ile	Lys	Val	Thr	Val	Glu	His	Pro	Asp	Lys	Leu	Glu	Glu	Lys	Phe	
			35					40					45			

cca	cag	gtt	gcg	gca	act	ggc	gat	ggc	cct	gac	att	atc	ttc	tgg	gca	192
Pro	Gln	Val	Ala	Ala	Thr	Gly	Asp	Gly	Pro	Asp	Ile	Ile	Phe	Trp	Ala	
			50					55					60			

cac	gac	cgc	ttt	ggt	ggc	tac	gct	caa	tct	ggc	ctg	ttg	gct	gaa	atc	240
His	Asp	Arg	Phe	Gly	Gly	Tyr	Ala	Gln	Ser	Gly	Leu	Leu	Ala	Glu	Ile	
			65				70				75				80	

acc	ccg	gac	aaa	gcg	ttc	cag	gac	aag	ctg	tat	ccg	ttt	acc	tgg	gat	288
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aaa ccg ttc gtt ggc gtg ctg agc gca ggt att aac gcc gcc agt ccg Lys Pro Phe Val Gly Val Leu Ser Ala Gly Ile Asn Ala Ala Ser Pro 260 265 270	816
aac aaa gag ctg gca aaa gag ttc ctc gaa aac tat ctg ctg act gat Asn Lys Glu Leu Ala Lys Glu Phe Leu Glu Asn Tyr Leu Leu Thr Asp 275 280 285	864
gaa ggt ctg gaa gcg gtt aat aaa gac aaa ccg ctg ggt gcc gta gcg Glu Gly Leu Glu Ala Val Asn Lys Asp Lys Pro Leu Gly Ala Val Ala 290 295 300	912
ctg aag tct tac gag gaa gag ttg gcg aaa gat cca cgt att gcc gcc Leu Lys Ser Tyr Glu Glu Glu Leu Ala Lys Asp Pro Arg Ile Ala Ala 305 310 315 320	960
acc atg gaa aac gcc cag aaa ggt gaa atc atg ccg aac atc ccg cag Thr Met Glu Asn Ala Gln Lys Gly Glu Ile Met Pro Asn Ile Pro Gln 325 330 335	1008
atg tcc gct ttc tgg tat gcc gtg cgt act gcg gtg atc aac gcc gcc Met Ser Ala Phe Trp Tyr Ala Val Arg Thr Ala Val Ile Asn Ala Ala 340 345 350	1056
agc ggt cgt cag act gtc gat gaa gcc ctg aaa gac gcg cag act aat Ser Gly Arg Gln Thr Val Asp Glu Ala Leu Lys Asp Ala Gln Thr Asn 355 360 365	1104
tcg agc tcc cac cat cac cat cac cac gcg aat tcg gta ccg ctg gtt Ser Ser Ser His His His His His His Ala Asn Ser Val Pro Leu Val 370 375 380	1152
ccg cgt gga tcc tgc ccc gac ctc gtc tgc tac acc gat tac ctc cag Pro Arg Gly Ser Cys Pro Asp Leu Val Cys Tyr Thr Asp Tyr Leu Gln 385 390 395 400	1200
acg gtc atc tgc atc ctg gaa atg tgg aac ctc cac ccc agc acg ctc Thr Val Ile Cys Ile Leu Glu Met Trp Asn Leu His Pro Ser Thr Leu 405 410 415	1248
acc ctt acc tgg caa gac cag tat gaa gag ctg aag gac gag gcc acc	1296

Thr	Leu	Thr	Trp	Gln	Asp	Gln	Tyr	Glu	Glu	Leu	Lys	Asp	Glu	Ala	Thr	
			420					425					430			
tcc	tgc	agc	ctc	cac	agg	tcg	gcc	cac	aat	gcc	acg	cat	gcc	acc	tac	1344
Ser	Cys	Ser	Leu	His	Arg	Ser	Ala	His	Asn	Ala	Thr	His	Ala	Thr	Tyr	
		435					440					445				
acc	tgc	cac	atg	gat	gta	ttc	cac	ttc	atg	gcc	gac	gac	att	ttc	agt	1392
Thr	Cys	His	Met	Asp	Val	Phe	His	Phe	Met	Ala	Asp	Asp	Ile	Phe	Ser	
	450					455					460					
gtc	aac	atc	aca	gac	cag	tct	ggc	aac	tac	tcc	cag	gag	tgt	ggc	agc	1440
Val	Asn	Ile	Thr	Asp	Gln	Ser	Gly	Asn	Tyr	Ser	Gln	Glu	Cys	Gly	Ser	
465					470					475					480	
ttt	ctc	ctg	gct	gag	agc	atc	aag	ccg	gct	ccc	cct	ttc	aac	gtg	act	1488
Phe	Leu	Leu	Ala	Glu	Ser	Ile	Lys	Pro	Ala	Pro	Pro	Phe	Asn	Val	Thr	
			485					490					495			
gtg	acc	ttc	tca	gga	cag	tat	aat	atc	tcc	tgg	cgc	tca	gat	tac	gaa	1536
Val	Thr	Phe	Ser	Gly	Gln	Tyr	Asn	Ile	Ser	Trp	Arg	Ser	Asp	Tyr	Glu	
		500					505					510				
gac	cct	gcc	ttc	tac	atg	ctg	aag	ggc	aag	ctt	cag	tat	gag	ctg	cag	1584
Asp	Pro	Ala	Phe	Tyr	Met	Leu	Lys	Gly	Lys	Leu	Gln	Tyr	Glu	Leu	Gln	
		515					520				525					
tac	agg	aac	cgg	gga	gac	ccc	tgg	gct	gtg	agt	ccg	agg	aga	aag	ctg	1632
Tyr	Arg	Asn	Arg	Gly	Asp	Pro	Trp	Ala	Val	Ser	Pro	Arg	Arg	Lys	Leu	
	530					535				540						
atc	tca	gtg	gac	tca	aga	agt	gtc	tcc	ctc	ctc	ccc	ctg	gag	ttc	cgc	1680
Ile	Ser	Val	Asp	Ser	Arg	Ser	Val	Ser	Leu	Leu	Pro	Leu	Glu	Phe	Arg	
545					550				555						560	
aaa	gac	tcg	agc	tat	gag	ctg	cag	gtg	cgg	gca	ggg	ccc	atg	cct	ggc	1728
Lys	Asp	Ser	Ser	Tyr	Glu	Leu	Gln	Val	Arg	Ala	Gly	Pro	Met	Pro	Gly	
			565					570					575			
tcc	tcc	tac	cag	ggg	acc	tgg	agt	gaa	tgg	agt	gac	ccg	gtc	atc	ttt	1776
Ser	Ser	Tyr	Gln	Gly	Thr	Trp	Ser	Glu	Trp	Ser	Asp	Pro	Val	Ile	Phe	
			580					585					590			

cag acc cag tca gag gag tta aag gaa ggc tgg aac cct cac tag 1821
 Gln Thr Gln Ser Glu Glu Leu Lys Glu Gly Trp Asn Pro His *
 595 600 605

<210> 30
 <211> 606
 <212> PRT
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 195 200 205
 Thr Asp Tyr Ser Ile Ala Glu Ala Ala Phe Asn Lys Gly Glu Thr Ala
 210 215 220
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 225 230 235 240
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 35 40 45

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Leu Asp Pro Glu Leu Leu Ser Ala Pro Gln Asp Val Lys Gly His Cys
50      55      60
Glu His Ala Ala Phe Ala Cys Phe Gln Lys Ala Lys Leu Lys Pro Ser
65      70      75      80
Asn Pro Gly Asn Asn Lys Thr Phe Ile Ile Asp Leu Val Ala Gln Leu
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Ala Lys Cys Pro Ser Cys Asp Ser Tyr Glu Lys Arg Thr Pro Lys Glu
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85 90 95

gac cag tat gaa gag ctg aag gac gag gcc acc tcc tgc agc ctc cac 336

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				245				250						255			
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Ser	Glu	Glu	Leu	Lys	Glu	Gly	Trp	Asn	Pro	His	Leu	Leu	Leu	Leu	Leu		
			260					265						270			

ctg Leu	ctt Leu	gtc Val 275	ata Ile	gtc Val	ttc Phe	att Ile	cct Pro	gcc Ala	ttc Phe	tgg Trp	agc Ser	ctg Leu	aag Lys	acc Thr	cat His	864
cca Pro	ttg Leu 290	tgg Trp	agg Arg	cta Leu	tgg Trp	aag Lys 295	aag Lys	ata Ile	tgg Trp	gcc Ala	gtc Val 300	ccc Pro	agc Ser	cct Pro	gag Glu	912
cgg Arg 305	ttc Phe	ttc Phe	atg Met	ccc Pro	ctg Leu 310	tac Tyr	aag Lys	ggc Gly	tgc Cys	agc Ser 315	gga Gly	gac Asp	ttc Phe	aag Lys	aaa Lys 320	960
tgg Trp	gtg Val	ggt Gly	gca Ala	ccc Pro 325	ttc Phe	act Thr	ggc Gly	tcc Ser	agc Ser 330	ctg Leu	gag Glu	ctg Leu	gga Gly	ccc Pro 335	tgg Trp	1008
agc Ser	cca Pro	gag Glu	gtg Val 340	ccc Pro	tcc Ser	acc Thr	ctg Leu	gag Glu	gtg Val	tac Tyr	agc Ser	tgc Cys	cac His	cca Pro	cca Pro	1056
cgg Arg	agc Ser	ccg Pro 355	gcc Ala	aag Lys	agg Arg	ctg Leu	cag Gln 360	ctc Leu	acg Thr	gag Glu	cta Leu	caa Gln 365	gaa Glu	cca Pro	gca Ala	1104
gag Glu	ctg Leu 370	gtg Val	gag Glu	tct Ser	gac Asp	ggc Gly 375	gtg Val	ccc Pro	aag Lys	ccc Pro	agc Ser 380	ttc Phe	tgg Trp	ccg Pro	aca Thr	1152
gcc Ala 385	cag Gln	aac Asn	tcg Ser	ggg Gly	ggc Gly 390	tca Ser	gct Ala	tac Tyr	agt Ser	gag Glu 395	gag Glu	agg Arg	gat Asp	cgg Arg	cca Pro 400	1200
tac Tyr	ggc Gly	ctg Leu	gtg Val	tcc Ser 405	att Ile	gac Asp	aca Thr	gtg Val	act Thr 410	gtg Val	cta Leu	gat Asp	gca Ala	gag Glu	ggg Gly	1248
cca Pro	tgc Cys	acc Thr 420	tgg Trp	ccc Pro	tgc Cys	agc Ser	tgt Cys	gag Glu 425	gat Asp	gac Asp	ggc Gly	tac Tyr 430	cca Pro	gcc Ala	ctg Leu	1296
gac Asp	ctg Leu	gat Asp 435	gct Ala	ggc Gly	ctg Leu	gag Glu	ccc Pro 440	agc Ser	cca Pro	ggc Gly	cta Leu	gag Glu 445	gac Asp	cca Pro	ctc Leu	1344

ttg gat gca ggg acc aca gtc ctg tcc tgt ggc tgt gtc tca gct ggc 1392
 Leu Asp Ala Gly Thr Thr Val Leu Ser Cys Gly Cys Val Ser Ala Gly
 450 455 460

agc cct ggg cta gga ggg ccc ctg gga agc ctc ctg gac aga cta aag 1440
 Ser Pro Gly Leu Gly Gly Pro Leu Gly Ser Leu Leu Asp Arg Leu Lys
 465 470 475 480

cca ccc ctt gca gat ggg gag gac tgg gct ggg gga ctg ccc tgg ggt 1488
 Pro Pro Leu Ala Asp Gly Glu Asp Trp Ala Gly Gly Leu Pro Trp Gly
 485 490 495

ggc cgg tca cct gga ggg gtc tca gag agt gag gcg ggc tca ccc ctg 1536
 Gly Arg Ser Pro Gly Gly Val Ser Glu Ser Glu Ala Gly Ser Pro Leu
 500 505 510

gcc ggc ctg gat atg gac acg ttt gac agt ggc ttt gtg ggc tct gac 1584
 Ala Gly Leu Asp Met Asp Thr Phe Asp Ser Gly Phe Val Gly Ser Asp
 515 520 525

tgc agc agc cct gtg gag tgt gac ttc acc agc ccc ggg gac gaa gga 1632
 Cys Ser Ser Pro Val Glu Cys Asp Phe Thr Ser Pro Gly Asp Glu Gly
 530 535 540

ccc ccc cgg agc tac ctc cgc cag tgg gtg gtc att cct ccg cca ctt 1680
 Pro Pro Arg Ser Tyr Leu Arg Gln Trp Val Val Ile Pro Pro Pro Leu
 545 550 555 560

tcg agc cct gga ccc cag gcc agc taa 1707
 Ser Ser Pro Gly Pro Gln Ala Ser *
 565

<210> 65

<211> 568

<212> PRT

<213> homo sapiens

<400> 65

Met Pro Arg Gly Trp Ala Ala Pro Leu Leu Leu Leu Leu Gln Gly
 1 5 10 15
 Ala Leu Glu Gly Met Glu Arg Lys Leu Cys Ser Pro Lys Pro Pro Pro
 20 25 30

Thr Lys Ala Ser Leu Pro Thr Asp Pro Pro Gly Trp Gly Cys Pro Asp
 35 40 45
 Leu Val Cys Tyr Thr Asp Tyr Leu Gln Thr Val Ile Cys Ile Leu Glu
 50 55 60
 Met Trp Asn Leu His Pro Ser Thr Leu Thr Leu Thr Trp Ile Leu Ser
 65 70 75 80
 Asn Asn Thr Gly Cys Tyr Ile Lys Asp Arg Thr Leu Asp Leu Arg Gln
 85 90 95
 Asp Gln Tyr Glu Glu Leu Lys Asp Glu Ala Thr Ser Cys Ser Leu His
 100 105 110
 Arg Ser Ala His Asn Ala Thr His Ala Thr Tyr Thr Cys His Met Asp
 115 120 125
 Val Phe His Phe Met Ala Asp Asp Ile Phe Ser Val Asn Ile Thr Asp
 130 135 140
 Gln Ser Gly Asn Tyr Ser Gln Glu Cys Gly Ser Phe Leu Leu Ala Glu
 145 150 155 160
 Ser Arg Gln Tyr Asn Ile Ser Trp Arg Ser Asp Tyr Glu Asp Pro Ala
 165 170 175
 Phe Tyr Met Leu Lys Gly Lys Leu Gln Tyr Glu Leu Gln Tyr Arg Asn
 180 185 190
 Arg Gly Asp Pro Trp Ala Val Ser Pro Arg Arg Lys Leu Ile Ser Val
 195 200 205
 Asp Ser Arg Ser Val Ser Leu Leu Pro Leu Glu Phe Arg Lys Asp Ser
 210 215 220
 Ser Tyr Glu Leu Gln Val Arg Ala Gly Pro Met Pro Gly Ser Ser Tyr
 225 230 235 240
 Gln Gly Thr Trp Ser Glu Trp Ser Asp Pro Val Ile Phe Gln Thr Gln
 245 250 255
 Ser Glu Glu Leu Lys Glu Gly Trp Asn Pro His Leu Leu Leu Leu Leu
 260 265 270
 Leu Leu Val Ile Val Phe Ile Pro Ala Phe Trp Ser Leu Lys Thr His
 275 280 285
 Pro Leu Trp Arg Leu Trp Lys Lys Ile Trp Ala Val Pro Ser Pro Glu
 290 295 300
 Arg Phe Phe Met Pro Leu Tyr Lys Gly Cys Ser Gly Asp Phe Lys Lys
 305 310 315 320
 Trp Val Gly Ala Pro Phe Thr Gly Ser Ser Leu Glu Leu Gly Pro Trp
 325 330 335
 Ser Pro Glu Val Pro Ser Thr Leu Glu Val Tyr Ser Cys His Pro Pro
 340 345 350
 Arg Ser Pro Ala Lys Arg Leu Gln Leu Thr Glu Leu Gln Glu Pro Ala
 355 360 365

Glu Leu Val Glu Ser Asp Gly Val Pro Lys Pro Ser Phe Trp Pro Thr
 370 375 380
 Ala Gln Asn Ser Gly Gly Ser Ala Tyr Ser Glu Glu Arg Asp Arg Pro
 385 390 395 400
 Tyr Gly Leu Val Ser Ile Asp Thr Val Thr Val Leu Asp Ala Glu Gly
 405 410 415
 Pro Cys Thr Trp Pro Cys Ser Cys Glu Asp Asp Gly Tyr Pro Ala Leu
 420 425 430
 Asp Leu Asp Ala Gly Leu Glu Pro Ser Pro Gly Leu Glu Asp Pro Leu
 435 440 445
 Leu Asp Ala Gly Thr Thr Val Leu Ser Cys Gly Cys Val Ser Ala Gly
 450 455 460
 Ser Pro Gly Leu Gly Gly Pro Leu Gly Ser Leu Leu Asp Arg Leu Lys
 465 470 475 480
 Pro Pro Leu Ala Asp Gly Glu Asp Trp Ala Gly Gly Leu Pro Trp Gly
 485 490 495
 Gly Arg Ser Pro Gly Gly Val Ser Glu Ser Glu Ala Gly Ser Pro Leu
 500 505 510
 Ala Gly Leu Asp Met Asp Thr Phe Asp Ser Gly Phe Val Gly Ser Asp
 515 520 525
 Cys Ser Ser Pro Val Glu Cys Asp Phe Thr Ser Pro Gly Asp Glu Gly
 530 535 540
 Pro Pro Arg Ser Tyr Leu Arg Gln Trp Val Val Ile Pro Pro Pro Leu
 545 550 555 560
 Ser Ser Pro Gly Pro Gln Ala Ser
 565

<210> 66

<211> 741

<212> DNA

<213> Artificial Sequence

<220>

<223> Degenerate polynucleotide sequence of SEQ ID NO:69

<221> misc_feature

<222> (1)...(741)

<223> n = A,T,C or G

<400> 66

atggarmgna arytnrgyws nccnaarccn ccnccnacna argcnwsnyt nccnacngay 60
 ccnccnggnt ggggntgycc ngayyngtn tgytayacng aytaytnca racngtnath 120

tgaythytn	aratgtggaa	yytncayccn	wsnacnytna	cnytnacntg	gathytwnsn	180
aayaayacng	gntgytayt	haargaymgn	acnytngayy	tnmgncarga	ycartaygar	240
garytnaarg	aygargcnac	nwsntgywsn	ytncaymgnw	sngcncayaa	ygcncncay	300
gcnacntaya	cntgycayt	ggaygtntty	cayttyatgg	cngaygayat	httywsngtn	360
aayathacng	aycarwsngg	naaytaywsn	cargartgyg	gnwsnttyyt	nytngcngar	420
wsnmgncart	ayaayathws	ntggmgnwsn	gaytaygarg	ayccngcntt	ytayatgytn	480
aarggnaary	tncartayga	rytncartay	mgnaaymgng	gngayccntg	ggcngtnwsn	540
ccnmgnmgna	arytnathws	ngtngaywsn	mgwnsngtnw	snytnytnc	nytngartty	600
mgnaargayw	snwsntayga	rytncargtn	mgngcnggnc	cnatgccngg	nwsnwsntay	660
carggnacnt	ggwsngartg	gwsngayccn	gtathhttyc	aracncarws	ngargarytn	720
aargarggnt	ggaayccnca	y				741

<210> 67

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> WXXW motif

<221> VARIANT

<222> (1)...(4)

<223> Xaa = Any Amino Acid

<400> 67

Trp Xaa Xaa Trp

1

<210> 68

<211> 741

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(741)

<400> 68

atg	gag	agg	aag	ctc	tgc	agt	ccc	aag	cca	ccc	ccc	acc	aag	gcc	tct	48
Met	Glu	Arg	Lys	Leu	Cys	Ser	Pro	Lys	Pro	Pro	Pro	Thr	Lys	Ala	Ser	
1				5					10					15		

ctc	ccc	act	gac	cct	cca	ggc	tgg	ggc	tgc	ccc	gac	ctc	gtc	tgc	tac	96
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	----

Leu	Pro	Thr	Asp	Pro	Pro	Gly	Trp	Gly	Cys	Pro	Asp	Leu	Val	Cys	Tyr	
			20					25					30			
acc	gat	tac	ctc	cag	acg	gtc	atc	tgc	atc	ctg	gaa	atg	tgg	aac	ctc	144
Thr	Asp	Tyr	Leu	Gln	Thr	Val	Ile	Cys	Ile	Leu	Glu	Met	Trp	Asn	Leu	
		35					40					45				
cac	ccc	agc	acg	ctc	acc	ctt	acc	tgg	ata	ctt	tct	aat	aat	act	ggg	192
His	Pro	Ser	Thr	Leu	Thr	Leu	Thr	Trp	Ile	Leu	Ser	Asn	Asn	Thr	Gly	
	50					55					60					
tgc	tat	atc	aag	gac	aga	aca	ctg	gac	ctc	agg	caa	gac	cag	tat	gaa	240
Cys	Tyr	Ile	Lys	Asp	Arg	Thr	Leu	Asp	Leu	Arg	Gln	Asp	Gln	Tyr	Glu	
65					70				75						80	
gag	ctg	aag	gac	gag	gcc	acc	tcc	tgc	agc	ctc	cac	agg	tcg	gcc	cac	288
Glu	Leu	Lys	Asp	Glu	Ala	Thr	Ser	Cys	Ser	Leu	His	Arg	Ser	Ala	His	
				85				90						95		
aat	gcc	acg	cat	gcc	acc	tac	acc	tgc	cac	atg	gat	gta	ttc	cac	ttc	336
Asn	Ala	Thr	His	Ala	Thr	Tyr	Thr	Cys	His	Met	Asp	Val	Phe	His	Phe	
			100					105					110			
atg	gcc	gac	gac	att	ttc	agt	gtc	aac	atc	aca	gac	cag	tct	ggc	aac	384
Met	Ala	Asp	Asp	Ile	Phe	Ser	Val	Asn	Ile	Thr	Asp	Gln	Ser	Gly	Asn	
		115					120					125				
tac	tcc	cag	gag	tgt	ggc	agc	ttt	ctc	ctg	gct	gag	agc	aga	cag	tat	432
Tyr	Ser	Gln	Glu	Cys	Gly	Ser	Phe	Leu	Leu	Ala	Glu	Ser	Arg	Gln	Tyr	
	130					135					140					
aat	atc	tcc	tgg	cgc	tca	gat	tac	gaa	gac	cct	gcc	ttc	tac	atg	ctg	480
Asn	Ile	Ser	Trp	Arg	Ser	Asp	Tyr	Glu	Asp	Pro	Ala	Phe	Tyr	Met	Leu	
145					150					155					160	
aag	ggc	aag	ctt	cag	tat	gag	ctg	cag	tac	agg	aac	cgg	gga	gac	ccc	528
Lys	Gly	Lys	Leu	Gln	Tyr	Glu	Leu	Gln	Tyr	Arg	Asn	Arg	Gly	Asp	Pro	
			165					170					175			
tgg	gct	gtg	agt	ccg	agg	aga	aag	ctg	atc	tca	gtg	gac	tca	aga	agt	576
Trp	Ala	Val	Ser	Pro	Arg	Arg	Lys	Leu	Ile	Ser	Val	Asp	Ser	Arg	Ser	
			180					185					190			

Met	Glu	Arg	Lys	Leu	Cys	Ser	Pro	Lys	Pro	Pro	Pro	Thr	Lys	Ala	Ser
1				5					10					15	
Leu	Pro	Thr	Asp	Pro	Pro	Gly	Trp	Gly	Cys	Pro	Asp	Leu	Val	Cys	Tyr
			20					25					30		
Thr	Asp	Tyr	Leu	Gln	Thr	Val	Ile	Cys	Ile	Leu	Glu	Met	Trp	Asn	Leu
		35					40					45			
His	Pro	Ser	Thr	Leu	Thr	Leu	Thr	Trp	Ile	Leu	Ser	Asn	Asn	Thr	Gly
	50					55					60				
Cys	Tyr	Ile	Lys	Asp	Arg	Thr	Leu	Asp	Leu	Arg	Gln	Asp	Gln	Tyr	Glu
65					70					75					80
Glu	Leu	Lys	Asp	Glu	Ala	Thr	Ser	Cys	Ser	Leu	His	Arg	Ser	Ala	His
				85					90					95	
Asn	Ala	Thr	His	Ala	Thr	Tyr	Thr	Cys	His	Met	Asp	Val	Phe	His	Phe
			100					105					110		
Met	Ala	Asp	Asp	Ile	Phe	Ser	Val	Asn	Ile	Thr	Asp	Gln	Ser	Gly	Asn
		115					120					125			
Tyr	Ser	Gln	Glu	Cys	Gly	Ser	Phe	Leu	Leu	Ala	Glu	Ser	Arg	Gln	Tyr
	130					135					140				
Asn	Ile	Ser	Trp	Arg	Ser	Asp	Tyr	Glu	Asp	Pro	Ala	Phe	Tyr	Met	Leu
145					150					155					160

Lys Gly Lys Leu Gln Tyr Glu Leu Gln Tyr Arg Asn Arg Gly Asp Pro
 165 170 175
 Trp Ala Val Ser Pro Arg Arg Lys Leu Ile Ser Val Asp Ser Arg Ser
 180 185 190
 Val Ser Leu Leu Pro Leu Glu Phe Arg Lys Asp Ser Ser Tyr Glu Leu
 195 200 205
 Gln Val Arg Ala Gly Pro Met Pro Gly Ser Ser Tyr Gln Gly Thr Trp
 210 215 220
 Ser Glu Trp Ser Asp Pro Val Ile Phe Gln Thr Gln Ser Glu Glu Leu
 225 230 235 240
 Lys Glu Gly Trp Asn Pro His
 245

<210> 70

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Domain linker motif; PAPP motif

<400> 70

Pro Ala Pro Pro

1

<210> 71

<211> 261

<212> PRT

<213> Artificial Sequence

<220>

<223> Representative variant soluble receptor with
domain linker

<221> VARIANT

<222> (1)...(261)

<223> Xaa = Any Amino Acid

<400> 71

Met Glu Arg Lys Leu Cys Ser Pro Lys Pro Pro Pro Thr Lys Ala Ser

1

5

10

15

Leu Pro Thr Asp Pro Pro Gly Trp Gly Cys Pro Asp Leu Val Cys Tyr
 20 25 30
 Thr Asp Tyr Leu Gln Thr Val Ile Cys Ile Leu Glu Met Trp Asn Leu
 35 40 45
 His Pro Ser Thr Leu Thr Leu Thr Trp Ile Leu Ser Asn Asn Thr Gly
 50 55 60
 Cys Tyr Ile Lys Asp Arg Thr Leu Asp Leu Arg Gln Asp Gln Tyr Glu
 65 70 75 80
 Glu Leu Lys Asp Glu Ala Thr Ser Cys Ser Leu His Arg Ser Ala His
 85 90 95
 Asn Ala Thr His Ala Thr Tyr Thr Cys His Met Asp Val Phe His Phe
 100 105 110
 Met Ala Asp Asp Ile Phe Ser Val Asn Ile Thr Asp Gln Ser Gly Asn
 115 120 125
 Tyr Ser Gln Glu Cys Gly Ser Phe Leu Leu Ala Glu Ser Xaa Xaa Pro
 130 135 140
 Ala Pro Pro Xaa Xaa Xaa Xaa Xaa Xaa Xaa Arg Gln Tyr Asn Ile
 145 150 155 160
 Ser Trp Arg Ser Asp Tyr Glu Asp Pro Ala Phe Tyr Met Leu Lys Gly
 165 170 175
 Lys Leu Gln Tyr Glu Leu Gln Tyr Arg Asn Arg Gly Asp Pro Trp Ala
 180 185 190
 Val Ser Pro Arg Arg Lys Leu Ile Ser Val Asp Ser Arg Ser Val Ser
 195 200 205
 Leu Leu Pro Leu Glu Phe Arg Lys Asp Ser Ser Tyr Glu Leu Gln Val
 210 215 220
 Arg Ala Gly Pro Met Pro Gly Ser Ser Tyr Gln Gly Thr Trp Ser Glu
 225 230 235 240
 Trp Ser Asp Pro Val Ile Phe Gln Thr Gln Ser Glu Glu Leu Lys Glu
 245 250 255
 Gly Trp Asn Pro His
 260

<210> 72

<211> 1461

<212> DNA

<213> Artificial Sequence

<220>

<223> Mouse zalphal1 extracellular domain murine
 immunoglobulin gamma 2a heavy chain Fc region
 fusion protein (zalphal1m-mG2a) Polynucleotide

<221> CDS

<222> (1)...(1461)

<400> 72

atg gat gca atg aag aga ggg ctc tgc tgt gtg ctg ctg ctg tgt ggc	48
Met Asp Ala Met Lys Arg Gly Leu Cys Cys Val Leu Leu Leu Cys Gly	
1 5 10 15	
gcc gtc ttc gtt tcg ctc agc cag aaa atc cat gcc gag ttg aga cgc	96
Ala Val Phe Val Ser Leu Ser Gln Lys Ile His Ala Glu Leu Arg Arg	
20 25 30	
ttc cgg aga tgc ctg gac ctc act tgc tac act gac tac ctc tgg acc	144
Phe Arg Arg Cys Leu Asp Leu Thr Cys Tyr Thr Asp Tyr Leu Trp Thr	
35 40 45	
atc acc tgt gtc ctg gag aca cgg agc ccc aac ccc agc ata ctc agt	192
Ile Thr Cys Val Leu Glu Thr Arg Ser Pro Asn Pro Ser Ile Leu Ser	
50 55 60	
ctc acc tgg caa gat gaa tat gag gaa ctt cag gac caa gag acc ttc	240
Leu Thr Trp Gln Asp Glu Tyr Glu Glu Leu Gln Asp Gln Glu Thr Phe	
65 70 75 80	
tgc agc cta cac agg tct ggc cac aac acc aca cat ata tgg tac acg	288
Cys Ser Leu His Arg Ser Gly His Asn Thr Thr His Ile Trp Tyr Thr	
85 90 95	
tgc cat atg cgc ttg tct caa ttc ctg tcc gat gaa gtt ttc att gtc	336
Cys His Met Arg Leu Ser Gln Phe Leu Ser Asp Glu Val Phe Ile Val	
100 105 110	
aat gtg acg gac cag tct ggc aac aac tcc caa gag tgt ggc agc ttt	384
Asn Val Thr Asp Gln Ser Gly Asn Asn Ser Gln Glu Cys Gly Ser Phe	
115 120 125	
gtc ctg gct gag agc atc aaa cca gct ccc ccc ttg aac gtg act gtg	432
Val Leu Ala Glu Ser Ile Lys Pro Ala Pro Pro Leu Asn Val Thr Val	
130 135 140	
gcc ttc tca gga cgc tat gat atc tcc tgg gac tca gct tat gac gaa	480

gtg gaa gta cac aca gct cag aca caa acc cat aga gag gat tac aac	1008
Val Glu Val His Thr Ala Gln Thr Gln Thr His Arg Glu Asp Tyr Asn	
325 330 335	
agt act ctc cgg gtg gtc agt gcc ctc ccc atc cag cac cag gac tgg	1056
Ser Thr Leu Arg Val Val Ser Ala Leu Pro Ile Gln His Gln Asp Trp	
340 345 350	
atg agt ggc aag gag ttc aaa tgc aag gtc aac aac aaa gac ctc cca	1104
Met Ser Gly Lys Glu Phe Lys Cys Lys Val Asn Asn Lys Asp Leu Pro	
355 360 365	
gcg ccc atc gag aga acc atc tca aaa ccc aaa ggg tca gta aga gct	1152
Ala Pro Ile Glu Arg Thr Ile Ser Lys Pro Lys Gly Ser Val Arg Ala	
370 375 380	
cca cag gta tat gtc ttg cct cca cca gaa gaa gag atg act aag aaa	1200
Pro Gln Val Tyr Val Leu Pro Pro Pro Glu Glu Glu Met Thr Lys Lys	
385 390 395 400	
cag gtc act ctg acc tgc atg gtc aca gac ttc atg cct gaa gac att	1248
Gln Val Thr Leu Thr Cys Met Val Thr Asp Phe Met Pro Glu Asp Ile	
405 410 415	
tac gtg gag tgg acc aac aac ggg aaa aca gag cta aac tac aag aac	1296
Tyr Val Glu Trp Thr Asn Asn Gly Lys Thr Glu Leu Asn Tyr Lys Asn	
420 425 430	
act gaa cca gtc ctg gac tct gat ggt tct tac ttc atg tac agc aag	1344
Thr Glu Pro Val Leu Asp Ser Asp Gly Ser Tyr Phe Met Tyr Ser Lys	
435 440 445	
ctg aga gtg gaa aag aag aac tgg gtg gaa aga aat agc tac tcc tgt	1392
Leu Arg Val Glu Lys Lys Asn Trp Val Glu Arg Asn Ser Tyr Ser Cys	
450 455 460	
tca gtg gtc cac gag ggt ctg cac aat cac cac acg act aag agc ttc	1440
Ser Val Val His Glu Gly Leu His Asn His His Thr Thr Lys Ser Phe	
465 470 475 480	
tcc cgg act ccg ggt aaa taa	1461

Ser Arg Thr Pro Gly Lys *
485

<210> 73
<211> 486
<212> PRT
<213> Artificial Sequence

<400> 73

Met	Asp	Ala	Met	Lys	Arg	Gly	Leu	Cys	Cys	Val	Leu	Leu	Leu	Cys	Gly
1				5				10						15	
Ala	Val	Phe	Val	Ser	Leu	Ser	Gln	Lys	Ile	His	Ala	Glu	Leu	Arg	Arg
			20					25					30		
Phe	Arg	Arg	Cys	Leu	Asp	Leu	Thr	Cys	Tyr	Thr	Asp	Tyr	Leu	Trp	Thr
		35				40					45				
Ile	Thr	Cys	Val	Leu	Glu	Thr	Arg	Ser	Pro	Asn	Pro	Ser	Ile	Leu	Ser
	50					55				60					
Leu	Thr	Trp	Gln	Asp	Glu	Tyr	Glu	Glu	Leu	Gln	Asp	Gln	Glu	Thr	Phe
65				70						75				80	
Cys	Ser	Leu	His	Arg	Ser	Gly	His	Asn	Thr	Thr	His	Ile	Trp	Tyr	Thr
			85					90				95			
Cys	His	Met	Arg	Leu	Ser	Gln	Phe	Leu	Ser	Asp	Glu	Val	Phe	Ile	Val
		100						105				110			
Asn	Val	Thr	Asp	Gln	Ser	Gly	Asn	Asn	Ser	Gln	Glu	Cys	Gly	Ser	Phe
		115				120					125				
Val	Leu	Ala	Glu	Ser	Ile	Lys	Pro	Ala	Pro	Pro	Leu	Asn	Val	Thr	Val
	130					135					140				
Ala	Phe	Ser	Gly	Arg	Tyr	Asp	Ile	Ser	Trp	Asp	Ser	Ala	Tyr	Asp	Glu
145				150						155				160	
Pro	Ser	Asn	Tyr	Val	Leu	Arg	Gly	Lys	Leu	Gln	Tyr	Glu	Leu	Gln	Tyr
			165					170						175	
Arg	Asn	Leu	Arg	Asp	Pro	Tyr	Ala	Val	Arg	Pro	Val	Thr	Lys	Leu	Ile
		180						185				190			
Ser	Val	Asp	Ser	Arg	Asn	Val	Ser	Leu	Leu	Pro	Glu	Glu	Phe	His	Lys
	195				200					205					
Asp	Ser	Ser	Tyr	Gln	Leu	Gln	Val	Arg	Ala	Ala	Pro	Gln	Pro	Gly	Thr
	210				215					220					
Ser	Phe	Arg	Gly	Thr	Trp	Ser	Glu	Trp	Ser	Asp	Pro	Val	Ile	Phe	Gln
225				230						235				240	
Thr	Gln	Ala	Gly	Glu	Pro	Glu	Ala	Gly	Trp	Asp	Pro	His	Glu	Pro	Arg
			245					250					255		

Ser Pro Thr Ile Lys Pro Cys Pro Pro Cys Lys Cys Pro Ala Pro Asn
 260 265 270
 Leu Leu Gly Gly Pro Ser Val Phe Ile Phe Pro Pro Lys Ile Lys Asp
 275 280 285
 Val Leu Met Ile Ser Leu Ser Pro Ile Val Thr Cys Val Val Val Asp
 290 295 300
 Val Ser Glu Asp Asp Pro Asp Val Gln Ile Ser Trp Phe Val Asn Asn
 305 310 315 320
 Val Glu Val His Thr Ala Gln Thr Gln Thr His Arg Glu Asp Tyr Asn
 325 330 335
 Ser Thr Leu Arg Val Val Ser Ala Leu Pro Ile Gln His Gln Asp Trp
 340 345 350
 Met Ser Gly Lys Glu Phe Lys Cys Lys Val Asn Asn Lys Asp Leu Pro
 355 360 365
 Ala Pro Ile Glu Arg Thr Ile Ser Lys Pro Lys Gly Ser Val Arg Ala
 370 375 380
 Pro Gln Val Tyr Val Leu Pro Pro Pro Glu Glu Glu Met Thr Lys Lys
 385 390 395 400
 Gln Val Thr Leu Thr Cys Met Val Thr Asp Phe Met Pro Glu Asp Ile
 405 410 415
 Tyr Val Glu Trp Thr Asn Asn Gly Lys Thr Glu Leu Asn Tyr Lys Asn
 420 425 430
 Thr Glu Pro Val Leu Asp Ser Asp Gly Ser Tyr Phe Met Tyr Ser Lys
 435 440 445
 Leu Arg Val Glu Lys Lys Asn Trp Val Glu Arg Asn Ser Tyr Ser Cys
 450 455 460
 Ser Val Val His Glu Gly Leu His Asn His His Thr Thr Lys Ser Phe
 465 470 475 480
 Ser Arg Thr Pro Gly Lys
 485

<210> 74

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer ZC26644

<400> 74

ggggtcgacg gccggccacc atg

<210> 75
 <211> 35
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide primer ZC26641

<400> 75
 caagtgaggt ccagcatct ccggaagcgt ctcaa 35

<210> 76
 <211> 35
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide primer ZC26642

<400> 76
 ttgagacgct tccggagatg cctggacctc acttg 35

<210> 77
 <211> 36
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide primer ZC26662

<400> 77
 tgtgggagat ctgggctcgt gaggggtccca gcctgc 36

<210> 78
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide primer ZC26643

<400> 78
 gagcccagat ctcccacaat caagccctgt 30

<210> 79
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide primer ZC26645

<400> 79
 aaacgcggcc gcggatccgg c 21

<210> 80
 <211> 35
 <212> PRT
 <213> Homo sapeins

<400> 80
 Met Asp Ala Met Lys Arg Gly Leu Cys Cys Val Leu Leu Leu Cys Gly
 1 5 10 15
 Ala Val Phe Val Ser Leu Ser Gln Glu Ile His Ala Glu Leu Arg Arg
 20 25 30
 Phe Arg Arg
 35

<210> 81
 <211> 966
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(966)

<400> 81
 ggg ggc ggg ggc gcc gcg cct acg gaa act cag cca cct gtg aca aat 48
 Gly Gly Gly Gly Ala Ala Pro Thr Glu Thr Gln Pro Pro Val Thr Asn
 1 5 10 15

ttg agt gtc tct gtt gaa aac ctc tgc aca gta ata tgg aca tgg aat 96
 Leu Ser Val Ser Val Glu Asn Leu Cys Thr Val Ile Trp Thr Trp Asn
 20 25 30

cca ccc gag gga gcc agc tca aat tgt agt cta tgg tat ttt agt cat	144
Pro Pro Glu Gly Ala Ser Ser Asn Cys Ser Leu Trp Tyr Phe Ser His	
35 40 45	
ttt ggc gac aaa caa gat aag aaa ata gct ccg gaa act cgt cgt tca	192
Phe Gly Asp Lys Gln Asp Lys Lys Ile Ala Pro Glu Thr Arg Arg Ser	
50 55 60	
ata gaa gta ccc ctg aat gag agg att tgt ctg caa gtg ggg tcc cag	240
Ile Glu Val Pro Leu Asn Glu Arg Ile Cys Leu Gln Val Gly Ser Gln	
65 70 75 80	
tgt agc acc aat gag agt gag aag cct agc att ttg gtt gaa aaa tgc	288
Cys Ser Thr Asn Glu Ser Glu Lys Pro Ser Ile Leu Val Glu Lys Cys	
85 90 95	
atc tca ccc cca gaa ggt gat cct gag tct gct gtg act gag ctt caa	336
Ile Ser Pro Pro Glu Gly Asp Pro Glu Ser Ala Val Thr Glu Leu Gln	
100 105 110	
tgc att tgg cac aac ctg agc tac atg aag tgt tct tgg ctc cct gga	384
Cys Ile Trp His Asn Leu Ser Tyr Met Lys Cys Ser Trp Leu Pro Gly	
115 120 125	
agg aat acc agt ccc gac act aac tat act ctc tac tat tgg cac aga	432
Arg Asn Thr Ser Pro Asp Thr Asn Tyr Thr Leu Tyr Tyr Trp His Arg	
130 135 140	
agc ctg gaa aaa att cat caa tgt gaa aac atc ttt aga gaa ggc caa	480
Ser Leu Glu Lys Ile His Gln Cys Glu Asn Ile Phe Arg Glu Gly Gln	
145 150 155 160	
tac ttt ggt tgt tcc ttt gat ctg acc aaa gtg aag gat tcc agt ttt	528
Tyr Phe Gly Cys Ser Phe Asp Leu Thr Lys Val Lys Asp Ser Ser Phe	
165 170 175	
gaa caa cac agt gtc caa ata atg gtc aag gat aat gca gga aaa att	576
Glu Gln His Ser Val Gln Ile Met Val Lys Asp Asn Ala Gly Lys Ile	
180 185 190	
aaa cca tcc ttc aat ata gtg cct tta act tcc cgt gtg aaa cct gat	624
Lys Pro Ser Phe Asn Ile Val Pro Leu Thr Ser Arg Val Lys Pro Asp	
195 200 205	

cct cca cat att aaa aac ctc tcc ttc cac aat gat gac cta tat gtg	672
Pro Pro His Ile Lys Asn Leu Ser Phe His Asn Asp Asp Leu Tyr Val	
210 215 220	
caa tgg gag aat cca cag aat ttt att agc aga tgc cta ttt tat gaa	720
Gln Trp Glu Asn Pro Gln Asn Phe Ile Ser Arg Cys Leu Phe Tyr Glu	
225 230 235 240	
gta gaa gtc aat aac agc caa act gag aca cat aat gtt ttc tac gtc	768
Val Glu Val Asn Asn Ser Gln Thr Glu Thr His Asn Val Phe Tyr Val	
245 250 255	
caa gag gct aaa tgt gag aat cca gaa ttt gag aga aat gtg gag aat	816
Gln Glu Ala Lys Cys Glu Asn Pro Glu Phe Glu Arg Asn Val Glu Asn	
260 265 270	
aca tct tgt ttc atg gtc cct ggt gtt ctt cct gat act ttg aac aca	864
Thr Ser Cys Phe Met Val Pro Gly Val Leu Pro Asp Thr Leu Asn Thr	
275 280 285	
gtc aga ata aga gtc aaa aca aat aag tta tgc tat gag gat gac aaa	912
Val Arg Ile Arg Val Lys Thr Asn Lys Leu Cys Tyr Glu Asp Asp Lys	
290 295 300	
ctc tgg agt aat tgg agc caa gaa atg agt ata ggt aag aag cgc aat	960
Leu Trp Ser Asn Trp Ser Gln Glu Met Ser Ile Gly Lys Lys Arg Asn	
305 310 315 320	
tcc aca	966
Ser Thr	

<210> 82

<211> 322

<212> PRT

<213> Homo sapiens

<400> 82

Gly Gly Gly Gly Ala Ala Pro Thr Glu Thr Gln Pro Pro Val Thr Asn
1 5 10 15
Leu Ser Val Ser Val Glu Asn Leu Cys Thr Val Ile Trp Thr Trp Asn
20 25 30

Pro Pro Glu Gly Ala Ser Ser Asn Cys Ser Leu Trp Tyr Phe Ser His
 35 40 45
 Phe Gly Asp Lys Gln Asp Lys Lys Ile Ala Pro Glu Thr Arg Arg Ser
 50 55 60
 Ile Glu Val Pro Leu Asn Glu Arg Ile Cys Leu Gln Val Gly Ser Gln
 65 70 75 80
 Cys Ser Thr Asn Glu Ser Glu Lys Pro Ser Ile Leu Val Glu Lys Cys
 85 90 95
 Ile Ser Pro Pro Glu Gly Asp Pro Glu Ser Ala Val Thr Glu Leu Gln
 100 105 110
 Cys Ile Trp His Asn Leu Ser Tyr Met Lys Cys Ser Trp Leu Pro Gly
 115 120 125
 Arg Asn Thr Ser Pro Asp Thr Asn Tyr Thr Leu Tyr Tyr Trp His Arg
 130 135 140
 Ser Leu Glu Lys Ile His Gln Cys Glu Asn Ile Phe Arg Glu Gly Gln
 145 150 155 160
 Tyr Phe Gly Cys Ser Phe Asp Leu Thr Lys Val Lys Asp Ser Ser Phe
 165 170 175
 Glu Gln His Ser Val Gln Ile Met Val Lys Asp Asn Ala Gly Lys Ile
 180 185 190
 Lys Pro Ser Phe Asn Ile Val Pro Leu Thr Ser Arg Val Lys Pro Asp
 195 200 205
 Pro Pro His Ile Lys Asn Leu Ser Phe His Asn Asp Asp Leu Tyr Val
 210 215 220
 Gln Trp Glu Asn Pro Gln Asn Phe Ile Ser Arg Cys Leu Phe Tyr Glu
 225 230 235 240
 Val Glu Val Asn Asn Ser Gln Thr Glu Thr His Asn Val Phe Tyr Val
 245 250 255
 Gln Glu Ala Lys Cys Glu Asn Pro Glu Phe Glu Arg Asn Val Glu Asn
 260 265 270
 Thr Ser Cys Phe Met Val Pro Gly Val Leu Pro Asp Thr Leu Asn Thr
 275 280 285
 Val Arg Ile Arg Val Lys Thr Asn Lys Leu Cys Tyr Glu Asp Asp Lys
 290 295 300
 Leu Trp Ser Asn Trp Ser Gln Glu Met Ser Ile Gly Lys Lys Arg Asn
 305 310 315 320
 Ser Thr

<210> 83

<211> 951

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(951)

<400> 83

gac acc gag ata aaa gtt aac cct cct cag gat ttt gag ata gtg gat	48
Asp Thr Glu Ile Lys Val Asn Pro Pro Gln Asp Phe Glu Ile Val Asp	
1 5 10 15	
ccc gga tac tta ggt tat ctc tat ttg caa tgg caa ccc cca ctg tct	96
Pro Gly Tyr Leu Gly Tyr Leu Tyr Leu Gln Trp Gln Pro Pro Leu Ser	
20 25 30	
ctg gat cat ttt aag gaa tgc aca gtg gaa tat gaa cta aaa tac cga	144
Leu Asp His Phe Lys Glu Cys Thr Val Glu Tyr Glu Leu Lys Tyr Arg	
35 40 45	
aac att ggt agt gaa aca tgg aag acc atc att act aag aat cta cat	192
Asn Ile Gly Ser Glu Thr Trp Lys Thr Ile Ile Thr Lys Asn Leu His	
50 55 60	
tac aaa gat ggg ttt gat ctt aac aag ggc att gaa gcg aag ata cac	240
Tyr Lys Asp Gly Phe Asp Leu Asn Lys Gly Ile Glu Ala Lys Ile His	
65 70 75 80	
acg ctt tta cca tgg caa tgc aca aat gga tca gaa gtt caa agt tcc	288
Thr Leu Leu Pro Trp Gln Cys Thr Asn Gly Ser Glu Val Gln Ser Ser	
85 90 95	
tgg gca gaa act act tat tgg ata tca cca caa gga att cca gaa act	336
Trp Ala Glu Thr Thr Tyr Trp Ile Ser Pro Gln Gly Ile Pro Glu Thr	
100 105 110	
aaa gtt cag gat atg gat tgc gta tat tac aat tgg caa tat tta ctc	384
Lys Val Gln Asp Met Asp Cys Val Tyr Tyr Asn Trp Gln Tyr Leu Leu	
115 120 125	
tgt tct tgg aaa cct ggc ata ggt gta ctt ctt gat acc aat tac aac	432
Cys Ser Trp Lys Pro Gly Ile Gly Val Leu Leu Asp Thr Asn Tyr Asn	
130 135 140	
ttg ttt tac tgg tat gag ggc ttg gat cat gca tta cag tgt gtt gat	480

Leu	Phe	Tyr	Trp	Tyr	Glu	Gly	Leu	Asp	His	Ala	Leu	Gln	Cys	Val	Asp	
145					150					155					160	
tac	atc	aag	gct	gat	gga	caa	aat	ata	gga	tgc	aga	ttt	ccc	tat	ttg	528
Tyr	Ile	Lys	Ala	Asp	Gly	Gln	Asn	Ile	Gly	Cys	Arg	Phe	Pro	Tyr	Leu	
				165					170					175		
gag	gca	tca	gac	tat	aaa	gat	ttc	tat	att	tgt	gtt	aat	gga	tca	tca	576
Glu	Ala	Ser	Asp	Tyr	Lys	Asp	Phe	Tyr	Ile	Cys	Val	Asn	Gly	Ser	Ser	
			180					185					190			
gag	aac	aag	cct	atc	aga	tcc	agt	tat	ttc	act	ttt	cag	ctt	caa	aat	624
Glu	Asn	Lys	Pro	Ile	Arg	Ser	Ser	Tyr	Phe	Thr	Phe	Gln	Leu	Gln	Asn	
		195					200					205				
ata	gtt	aaa	cct	ttg	ccg	cca	gtc	tat	ctt	act	ttt	act	cgg	gag	agt	672
Ile	Val	Lys	Pro	Leu	Pro	Pro	Val	Tyr	Leu	Thr	Phe	Thr	Arg	Glu	Ser	
	210					215					220					
tca	tgt	gaa	att	aag	ctg	aaa	tgg	agc	ata	cct	ttg	gga	cct	att	cca	720
Ser	Cys	Glu	Ile	Lys	Leu	Lys	Trp	Ser	Ile	Pro	Leu	Gly	Pro	Ile	Pro	
225					230				235						240	
gca	agg	tgt	ttt	gat	tat	gaa	att	gag	atc	aga	gaa	gat	gat	act	acc	768
Ala	Arg	Cys	Phe	Asp	Tyr	Glu	Ile	Glu	Ile	Arg	Glu	Asp	Asp	Thr	Thr	
			245						250					255		
ttg	gtg	act	gct	aca	gtt	gaa	aat	gaa	aca	tac	acc	ttg	aaa	aca	aca	816
Leu	Val	Thr	Ala	Thr	Val	Glu	Asn	Glu	Thr	Tyr	Thr	Leu	Lys	Thr	Thr	
			260					265					270			
aat	gaa	acc	cga	caa	tta	tgc	ttt	gta	gta	aga	agc	aaa	gtg	aat	att	864
Asn	Glu	Thr	Arg	Gln	Leu	Cys	Phe	Val	Val	Arg	Ser	Lys	Val	Asn	Ile	
		275					280					285				
tat	tgc	tca	gat	gac	gga	att	tgg	agt	gag	tgg	agt	gat	aaa	caa	tgc	912
Tyr	Cys	Ser	Asp	Asp	Gly	Ile	Trp	Ser	Glu	Trp	Ser	Asp	Lys	Gln	Cys	
	290					295					300					
tgg	gaa	ggt	gaa	gac	cta	tcg	aag	aaa	act	ttg	cta	cgt				951
Trp	Glu	Gly	Glu	Asp	Leu	Ser	Lys	Lys	Thr	Leu	Leu	Arg				
305					310				315							

<210> 84
 <211> 317
 <212> PRT
 <213> Homo sapiens

<400> 84

Asp	Thr	Glu	Ile	Lys	Val	Asn	Pro	Pro	Gln	Asp	Phe	Glu	Ile	Val	Asp
1				5					10					15	
Pro	Gly	Tyr	Leu	Gly	Tyr	Leu	Tyr	Leu	Gln	Trp	Gln	Pro	Pro	Leu	Ser
			20					25					30		
Leu	Asp	His	Phe	Lys	Glu	Cys	Thr	Val	Glu	Tyr	Glu	Leu	Lys	Tyr	Arg
		35					40					45			
Asn	Ile	Gly	Ser	Glu	Thr	Trp	Lys	Thr	Ile	Ile	Thr	Lys	Asn	Leu	His
		50				55					60				
Tyr	Lys	Asp	Gly	Phe	Asp	Leu	Asn	Lys	Gly	Ile	Glu	Ala	Lys	Ile	His
65					70					75				80	
Thr	Leu	Leu	Pro	Trp	Gln	Cys	Thr	Asn	Gly	Ser	Glu	Val	Gln	Ser	Ser
				85					90					95	
Trp	Ala	Glu	Thr	Thr	Tyr	Trp	Ile	Ser	Pro	Gln	Gly	Ile	Pro	Glu	Thr
			100					105					110		
Lys	Val	Gln	Asp	Met	Asp	Cys	Val	Tyr	Tyr	Asn	Trp	Gln	Tyr	Leu	Leu
		115					120					125			
Cys	Ser	Trp	Lys	Pro	Gly	Ile	Gly	Val	Leu	Leu	Asp	Thr	Asn	Tyr	Asn
		130				135						140			
Leu	Phe	Tyr	Trp	Tyr	Glu	Gly	Leu	Asp	His	Ala	Leu	Gln	Cys	Val	Asp
145					150					155					160
Tyr	Ile	Lys	Ala	Asp	Gly	Gln	Asn	Ile	Gly	Cys	Arg	Phe	Pro	Tyr	Leu
				165					170					175	
Glu	Ala	Ser	Asp	Tyr	Lys	Asp	Phe	Tyr	Ile	Cys	Val	Asn	Gly	Ser	Ser
			180						185					190	
Glu	Asn	Lys	Pro	Ile	Arg	Ser	Ser	Tyr	Phe	Thr	Phe	Gln	Leu	Gln	Asn
		195					200					205			
Ile	Val	Lys	Pro	Leu	Pro	Pro	Val	Tyr	Leu	Thr	Phe	Thr	Arg	Glu	Ser
		210				215						220			
Ser	Cys	Glu	Ile	Lys	Leu	Lys	Trp	Ser	Ile	Pro	Leu	Gly	Pro	Ile	Pro
225					230					235				240	
Ala	Arg	Cys	Phe	Asp	Tyr	Glu	Ile	Glu	Ile	Arg	Glu	Asp	Asp	Thr	Thr
				245						250				255	
Leu	Val	Thr	Ala	Thr	Val	Glu	Asn	Glu	Thr	Tyr	Thr	Leu	Lys	Thr	Thr
			260					265					270		
Asn	Glu	Thr	Arg	Gln	Leu	Cys	Phe	Val	Val	Arg	Ser	Lys	Val	Asn	Ile
		275					280						285		

Tyr Cys Ser Asp Asp Gly Ile Trp Ser Glu Trp Ser Asp Lys Gln Cys
 290 295 300
 Trp Glu Gly Glu Asp Leu Ser Lys Lys Thr Leu Leu Arg
 305 310 315

<210> 85
 <211> 519
 <212> DNA
 <213> Homo sapeins

<220>
 <221> CDS
 <222> (1)...(519)

<400> 85

atc acg tgc cct ccc ccc atg tcc gtg gaa cac gca gac atc tgg gtc 48
 Ile Thr Cys Pro Pro Pro Met Ser Val Glu His Ala Asp Ile Trp Val
 1 5 10 15

aag agc tac agc ttg tac tcc agg gag cgg tac att tgt aac tct ggt 96
 Lys Ser Tyr Ser Leu Tyr Ser Arg Glu Arg Tyr Ile Cys Asn Ser Gly
 20 25 30

ttc aag cgt aaa gcc ggc acg tcc agc ctg acg gag tgc gtg ttg aac 144
 Phe Lys Arg Lys Ala Gly Thr Ser Ser Leu Thr Glu Cys Val Leu Asn
 35 40 45

aag gcc acg aat gtc gcc cac tgg aca acc ccc agt ctc aaa tgc att 192
 Lys Ala Thr Asn Val Ala His Trp Thr Thr Pro Ser Leu Lys Cys Ile
 50 55 60

aga gac cct gcc ctg gtt cac caa agg cca gcg cca ccc tcc aca gta 240
 Arg Asp Pro Ala Leu Val His Gln Arg Pro Ala Pro Pro Ser Thr Val
 65 70 75 80

acg acg gca ggg gtg acc cca cag cca gag agc ctc tcc cct tct gga 288
 Thr Thr Ala Gly Val Thr Pro Gln Pro Glu Ser Leu Ser Pro Ser Gly
 85 90 95

aaa gag ccc gca gct tca tct ccc agc tca aac aac aca gcg gcc aca 336
 Lys Glu Pro Ala Ala Ser Ser Pro Ser Ser Asn Asn Thr Ala Ala Thr
 100 105 110

aca gca gct att gtc ccg ggc tcc cag ctg atg cct tca aaa tca cct 384
 Thr Ala Ala Ile Val Pro Gly Ser Gln Leu Met Pro Ser Lys Ser Pro
 115 120 125

tcc aca gga acc aca gag ata agc agt cat gag tcc tcc cac ggc acc 432
 Ser Thr Gly Thr Thr Glu Ile Ser Ser His Glu Ser Ser His Gly Thr
 130 135 140

ccc tct cag aca aca gcc aag aac tgg gaa ctc aca gca tcc gcc tcc 480
 Pro Ser Gln Thr Thr Ala Lys Asn Trp Glu Leu Thr Ala Ser Ala Ser
 145 150 155 160

cac cag ccg cca ggt gtg tat cca cag ggc cac agc gac 519
 His Gln Pro Pro Gly Val Tyr Pro Gln Gly His Ser Asp
 165 170

<210> 86

<211> 173

<212> PRT

<213> Homo sapeins

<400> 86

Ile Thr Cys Pro Pro Pro Met Ser Val Glu His Ala Asp Ile Trp Val
 1 5 10 15
 Lys Ser Tyr Ser Leu Tyr Ser Arg Glu Arg Tyr Ile Cys Asn Ser Gly
 20 25 30
 Phe Lys Arg Lys Ala Gly Thr Ser Ser Leu Thr Glu Cys Val Leu Asn
 35 40 45
 Lys Ala Thr Asn Val Ala His Trp Thr Thr Pro Ser Leu Lys Cys Ile
 50 55 60
 Arg Asp Pro Ala Leu Val His Gln Arg Pro Ala Pro Pro Ser Thr Val
 65 70 75 80
 Thr Thr Ala Gly Val Thr Pro Gln Pro Glu Ser Leu Ser Pro Ser Gly
 85 90 95
 Lys Glu Pro Ala Ala Ser Ser Pro Ser Ser Asn Asn Thr Ala Ala Thr
 100 105 110
 Thr Ala Ala Ile Val Pro Gly Ser Gln Leu Met Pro Ser Lys Ser Pro
 115 120 125
 Ser Thr Gly Thr Thr Glu Ile Ser Ser His Glu Ser Ser His Gly Thr
 130 135 140
 Pro Ser Gln Thr Thr Ala Lys Asn Trp Glu Leu Thr Ala Ser Ala Ser
 145 150 155 160

His Gln Pro Pro Gly Val Tyr Pro Gln Gly His Ser Asp
165 170

165 170
His Gln Pro Pro Gly Val Tyr Pro Gln Gly His Ser Asp
165 170